

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 22, 2005, 20:39:17 ; Search time 42 Seconds  
(without alignments)  
31.992 Million cell updates/sec

Title: US-10-721-839-32

Sequence: 1 GICRCICRGRCICGR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	91.3	18	US-10-141-645-6	Sequence 6, Appl1
2	102	88.7	18	US-10-141-645-1	Sequence 1, Appl1
3	99	86.1	18	US-10-141-645-2	Sequence 2, Appl1
4	97	84.3	18	US-10-141-645-3	Sequence 3, Appl1
5	97	84.3	18	US-10-141-645-4	Sequence 4, Appl1
6	97	84.3	18	US-10-141-645-5	Sequence 5, Appl1
7	95	82.6	18	US-10-141-645-7	Sequence 7, Appl1
8	88	76.5	18	US-09-309-487-1	Sequence 1, Appl1
9	88	76.5	18	US-09-309-487-8	Sequence 1, Appl1
10	87	75.7	18	US-10-141-645-8	Sequence 8, Appl1
11	87	75.7	18	US-10-141-645-9	Sequence 9, Appl1
12	86	74.8	18	US-09-917-340-53	Sequence 53, Appl1
13	85	73.9	18	US-09-309-487-9	Sequence 9, Appl1
14	85	73.9	18	US-09-309-487-14	Sequence 14, Appl1
15	85	73.9	18	US-09-309-487-29	Sequence 29, Appl1
16	73	63.5	92	US-09-309-487-21	Sequence 21, Appl1
17	64	55.7	76	US-09-309-487-14	Sequence 14, Appl1
18	64	55.7	76	US-09-309-487-29	Sequence 29, Appl1
19	64	55.7	76	US-09-309-487-14	Sequence 14, Appl1
20	64	55.7	76	US-09-309-487-29	Sequence 29, Appl1
21	64	55.7	76	US-10-141-645-15	Sequence 15, Appl1
22	61	53.0	180	US-09-510-238A-286	Sequence 286, App
23	61	53.0	2732	US-09-086-436-30	Sequence 30, Appl1
24	58	50.4	9	US-09-309-487-18	Sequence 18, Appl1
25	58	50.4	9	US-09-309-487-18	Sequence 18, Appl1
26	58	50.4	9	US-10-141-645-36	Sequence 36, Appl1
27	56	48.7	9	US-10-141-645-49	Sequence 49, Appl1

28	55.5	48.3	2211	3	US-09-738-884-1	Sequence 1, Appl1
29	55.5	48.3	2211	4	US-10-096-961A-1	Sequence 1, Appl1
30	55	47.8	1417	3	US-08-900-230-3	Sequence 3, Appl1
31	54	47.0	14	2	US-08-685-589A-157	Sequence 157, App
32	54	47.0	70	3	US-09-188-930-131	Sequence 131, App
33	54	47.0	70	4	US-09-312-283C-131	Sequence 32502, A
34	54	47.0	168	4	US-09-252-991A-32502	Sequence 156, App
35	53	46.1	14	2	US-08-685-589A-156	Sequence 159, App
36	53	46.1	14	3	US-09-604-864-8	Sequence 8, Appl1
37	53	46.1	18	3	US-09-604-864-9	Sequence 9, Appl1
38	53	46.1	18	4	US-10-042-872-8	Sequence 8, Appl1
39	53	46.1	18	4	US-10-042-872-9	Sequence 9, Appl1
40	53	46.1	18	4	US-10-042-872-9	Sequence 9, Appl1
41	52.5	45.7	1345	2	US-08-977-767-3	Sequence 3, Appl1
42	52	45.2	9	4	US-10-141-645-22	Sequence 22, Appl1
43	52	45.2	9	4	US-10-141-645-34	Sequence 34, Appl1
44	52	45.2	1652	4	US-09-627-650B-1	Sequence 1, Appl1
45	52	45.2	1652	4	US-09-436-063C-1	Sequence 1, Appl1

#### ALIGNMENTS

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RESULT 1
US-10-141-645-6
; Sequence 6, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Marling
; APPLICANT: Teresa Hong
; APPLICANT: Alexander Cole
; TITLE OF INVENTION: Retrocycling - Antiviral and
; FILE REFERENCE: Antimicrobial Peptides
; CURRENT APPLICATION NUMBER: US/10/141,645
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
US-10-141-645-6

Query Match          91.3%; Score 105; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.2e-06;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy      1  GICRCICRGRCICGR 18
Db      1  GICRCICRGRCICGR 18

RESULT 2
US-10-141-645-1
; Sequence 1, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Marling
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocycling - Antiviral and
; FILE REFERENCE: Antimicrobial Peptides
; CURRENT APPLICATION NUMBER: US/10/141,645
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; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: prt
; ORGANISM: Homo sapiens
; US-10-141-645-1
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Query Match      88.7%; Score 102; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.2e-06;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy      1 GICRCITRGFCRCICGR 18
Db      1 GICRCICGRCICRCICGR 18
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RESULT 3
US-10-141-645-2
; Sequence 2, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: prt
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
; US-10-141-645-2
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Query Match      86.1%; Score 99; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 2e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy      1 GICRCITRGFCRCICGR 18
Db      1 GICRCICGRCICRCICGR 18
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RESULT 4
US-10-141-645-3
; Sequence 3, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
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; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: prt
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
; US-10-141-645-3
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Query Match      84.3%; Score 97; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.4e-05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy      1 GICRCITRGFCRCICGR 18
Db      1 GICRCICGRCICRCICGR 18
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RESULT 5
US-10-141-645-4
; Sequence 4, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: prt
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
; US-10-141-645-4
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Query Match      84.3%; Score 97; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.4e-05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy      1 GICRCITRGFCRCICGR 18
Db      1 GICRCICGRCICRCICGR 18
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RESULT 6
US-10-141-645-5
; Sequence 5, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
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; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
US-10-141-645-5
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Query Match      84.3%; Score 97; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 3,4e-05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      1 GICRCICTRGFCRCICGR 18
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Db      1 GYCRCICGRCICRCICGR 18
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RESULT 7
US-10-141-645-7
; Sequence 7, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
US-10-141-645-7
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Query Match      82.6%; Score 95; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 5,7e-05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      1 GICRCICTRGFCRCICGR 18
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Db      1 GICRCICGRCICRCICGR 18
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RESULT 8
US-09-309-487-1
; Sequence 1, Application US/09309487
; Patent No. 6335318
; GENERAL INFORMATION:
; APPLICANT: Seisted, Michael E.
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Yuan, Jun
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
; FILE REFERENCE: P-UC 3095
; CURRENT APPLICATION NUMBER: US/09/309,487
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; CURRENT FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-309-487-1
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Query Match      76.5%; Score 88; DB 3; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.00036;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY      1 GICRCICTRGFCRCICGR 18
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Db      1 GFCRCICRGVCRCICCTR 18
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RESULT 9
US-09-967-808-1
; Sequence 1, Application US/09967808
; Patent No. 6514727
; GENERAL INFORMATION:
; APPLICANT: Seisted, Michael E.
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Yuan, Jun
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
; FILE REFERENCE: P-UC 3095
; CURRENT APPLICATION NUMBER: US/09/967,808
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US/09/309,487
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-967-808-1
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Query Match      76.5%; Score 88; DB 4; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.00036;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY      1 GICRCICTRGFCRCICGR 18
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Db      1 GFCRCICRGVCRCICCTR 18
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RESULT 10
US-10-141-645-8
; Sequence 8, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 18
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TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic variant  
US-10-141-645-8

Query Match 75.7%; Score 87; DB 4; Length 18;  
Best Local Similarity 77.8%; Pred. No. 0.00046;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18  
DB 1 GICICIGYGCRCICGR 18

RESULT 11  
US-10-141-645-9  
Sequence 9, Application US/10141645  
Patent No. 6713078  
GENERAL INFORMATION:  
APPLICANT: Robert Lehrer  
APPLICANT: Alan Maring  
APPLICANT: Alexander Cole  
APPLICANT: Teresa Hong  
TITLE OF INVENTION: Retrocyclins - Antiviral and  
FILE REFERENCE: UCLA-001CIP  
CURRENT APPLICATION NUMBER: US/10/141,645  
CURRENT FILING DATE: 2002-05-06  
PRIOR APPLICATION NUMBER: 60/284,855  
PRIOR FILING DATE: 2001-04-18  
PRIOR APPLICATION NUMBER: Unassigned  
PRIOR FILING DATE: 2002-04-18  
NUMBER OF SEQ ID NOS: 125  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic variant  
US-10-141-645-9

Query Match 75.7%; Score 87; DB 4; Length 18;  
Best Local Similarity 77.8%; Pred. No. 0.00046;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18  
DB 1 GICICIGYGCRCICGR 18

RESULT 12  
US-09-917-340-53  
Sequence 53, Application US/09917340  
Patent No. 6696238  
GENERAL INFORMATION:  
APPLICANT: Murphy, Christopher J.  
APPLICANT: McAnulty, Jonathan F.  
APPLICANT: Reid, Ted W.  
TITLE OF INVENTION: Transplant Media  
FILE REFERENCE: TPLANT-06468  
CURRENT APPLICATION NUMBER: US/09/917,340  
CURRENT FILING DATE: 2001-07-29  
PRIOR APPLICATION NUMBER: 60/221,632  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: 60/249,602  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/290,932  
PRIOR FILING DATE: 2001-05-15  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 53

LENGTH: 18  
TYPE: PRT  
ORGANISM: Macaca mulatta  
US-09-917-340-53

Query Match 74.8%; Score 86; DB 4; Length 18;  
Best Local Similarity 86.7%; Pred. No. 0.0006;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RCICTRGFCRCICGR 18  
DB 1 RCICTRGFCRCICGR 15

RESULT 13  
US-09-309-487-9  
Sequence 9, Application US/09309487  
Patent No. 6353318  
GENERAL INFORMATION:  
APPLICANT: Selsted, Michael E.  
APPLICANT: Tang, Yi-Quan  
APPLICANT: Yuan, Jun  
APPLICANT: Ouellette, Andre J.  
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same  
FILE REFERENCE: P-UC 3095  
CURRENT APPLICATION NUMBER: US/09/309,487  
CURRENT FILING DATE: 1999-05-10  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Macaca mulatta  
US-09-309-487-9

Query Match 73.9%; Score 85; DB 3; Length 18;  
Best Local Similarity 75.0%; Pred. No. 0.00078;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCIC 16  
DB 3 GFCRCICRGVCRIC 18

RESULT 14  
US-09-967-808-9  
Sequence 9, Application US/09967808  
Patent No. 6514727  
GENERAL INFORMATION:  
APPLICANT: Selsted, Michael E.  
APPLICANT: Tang, Yi-Quan  
APPLICANT: Yuan, Jun  
APPLICANT: Ouellette, Andre J.  
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using  
FILE REFERENCE: P-UC 3095  
CURRENT APPLICATION NUMBER: US/09/967,808  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: US/09/309,487  
PRIOR FILING DATE: 1999-05-10  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Macaca mulatta  
US-09-967-808-9

Query Match 73.9%; Score 85; DB 4; Length 18;  
Best Local Similarity 75.0%; Pred. No. 0.00078;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCIC 16

Db 3 GFCRCRCRGVCRCIC 18

RESULT 15  
US-09-309-487-21  
/ Sequence 21, Application US/09309487  
/ Patent No. 6335318  
/ GENERAL INFORMATION:  
/ APPLICANT: Selsted, Michael E.  
/ APPLICANT: Tang, Yi-Quan  
/ APPLICANT: Yuen, Jun  
/ APPLICANT: Ouellette, Andre J.  
/ TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same  
/ FILE REFERENCE: P-UC 3095  
/ CURRENT APPLICATION NUMBER: US/09/309,487  
/ CURRENT FILING DATE: 1999-05-10  
/ NUMBER OF SEQ ID NOS: 31  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 21  
/ LENGTH: 92  
/ TYPE: PRT  
/ ORGANISM: Macaca mulatta  
US-09-309-487-21

Query Match 63.5%; Score 73; DB 3; Length 92;  
Best Local Similarity 84.6%; Pred. No. 0.064;  
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RCICTRGFCRCIC 16  
Db 65 RCICTRGFCRLC 77

Search completed: March 22, 2005, 20:51:17  
Job time : 43 secs

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XX OS Homo sapiens.  
 XX PN WO2004033479-A2.  
 XX PD 22-APR-2004.  
 XX PF 06-MAY-2003; 2003WO-US014106.  
 XX PR 06-MAY-2002; 2002US-00141645.  
 XX (BEGC ) UNIV CALIFORNIA.  
 PA (LEHRER/) LEHRER R I.  
 PA (WARI/) WARING A J.  
 PA (COLE/) COLE A M.  
 PA (HONG/) HONG T B.  
 XX  
 PI Lehrer RI, Waring AJ, Cole AM, Hong TB;  
 DR WPI; 2004-340883/31.  
 DR N-PSDB; ADN08193.  
 XX  
 PT New isolated retrocyclin peptides and cyclic polypeptides, useful as  
 PT therapeutic and prophylactic agents for treating and preventing microbial  
 PT and viral infections.  
 PS  
 PS Claim 9; SEQ ID NO 1; 82pp; English.  
 CC The invention relates to a novel isolated retrocyclin peptide. The  
 CC invention further provides: a cyclic polypeptide; an isolated nucleic  
 CC acid encoding a primate retrocyclin; a method for preventing retroviral  
 CC infection in a cell by administering an effective dose of a circular  
 CC minidensin or retrocyclin to the cell; a method for killing microbial  
 CC organisms by administering an effective dose of retrocyclin to the  
 CC microbial organisms; a method for administering retrocyclin as a  
 CC therapeutic agent to a patient with an established microbial or viral  
 CC infection; and a method for administering retrocyclin as a prophylactic  
 CC agent to prevent a microbial or viral infection in a patient at risk of  
 CC developing such infection. The retrocyclin peptide has antibacterial and  
 CC virucide activities. The retrocyclin peptide can be used to treat a viral  
 CC infection such as HIV-1. The retrocyclin peptide can be used as a vaccine  
 CC and can be used in immunotherapy. The peptide and polypeptides are useful  
 CC as therapeutic and prophylactic agents for treating and preventing  
 CC microbial and viral infections. This sequence represents a retrocyclin  
 CC peptide of the invention.  
 CC  
 SQ Sequence 18 AA;  
 Query Match 88.7%; Score 102; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 0.00044;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GICRCICTRGFCRCICGR 18  
 DB 1 GICRCICGRGICRCICGR 18  
 RESULT 13  
 AAB53298  
 ID AAB53298 standard; peptide; 18 AA.  
 AC AAB53298;  
 XX  
 XX 13-NOV-2002 (first entry)  
 DT  
 XX Anti-viral chimeric theta defensin peptide H/RTD-3 SEQ ID NO:31.  
 XX  
 XX Anti-viral; viral infection; theta-defensin; lipid environment;  
 KW amphipathic alpha-helical structure; virucide; anti-HIV; immunisation;  
 KW viral growth inhibitor; viral proliferation inhibitor.  
 XX  
 XX Homo sapiens.  
 OS Macaca mulatta.

OS Synthetic.  
 XX PN WO200260468-A2.  
 XX PD 08-AUG-2002.  
 XX PF 29-JAN-2002; 2002WO-US002435.  
 XX PR 30-JAN-2001; 2001US-0265270P.  
 XX PR 01-AUG-2001; 2001US-0309368P.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA  
 PI Maury W, Stapleton J, Stinski M, Roller R, McCreary PB, Tack B;  
 DR WPI; 2002-674815/72.  
 XX  
 PT New method of using a first anti-viral peptide comprising a Theta-  
 PT defensin peptide in an amphipathic Alpha-helical structure in a lipid  
 PT environment for reducing the infectivity of a virus.  
 PS  
 PS Disclosure; Page 10; 65pp; English.  
 CC The present invention describes a method (M1) of using a first anti-viral  
 CC peptide (I) comprising a theta-defensin peptide in an amphipathic alpha  
 CC helical structure in a lipid environment for reducing the infectivity of  
 CC a virus. (I) can have virucide and anti-HIV activities, and can be used  
 CC to reduce virus growth, infectivity burden, shed, and development of anti  
 CC -viral resistance. (I) can be used for inhibiting the growth and  
 CC proliferation of a virus and so can be used for: (a) protecting or  
 CC treating subject from a viral infection, preventing recurrent viral  
 CC infection in a subject harbouring a latent virus, controlling viral  
 CC spread within a virally-infected subject (VS), reducing viral burden in a  
 CC VS, reducing virus shed from a VS, reducing percentage of VS in a  
 CC population regardless of viral infection status, or inducing latency in a  
 CC VS; (b) reducing the infectivity of a virus; and (c) reducing virus-  
 CC contaminated tissue or fluid sample safe for use, or reducing the number  
 CC of infectious virus particles in a population of viruses. (M1) is useful  
 CC for reducing the infectivity of a virus in sheep, cattle, horses, swine,  
 CC cats, fowl and humans e.g. an enveloped virus infecting humans such as  
 CC human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is  
 CC administered to a patient who is immunosuppressed or to a subject who is  
 CC not infected with the virus, where the first anti-viral peptide is  
 CC administered prior to or subsequent to the virus contacting the subject.  
 CC The anti-viral peptide is most preferably administered to a subject who  
 CC is chronically, latently or acutely infected with the virus. The present  
 CC sequence represents a chimeric human/rhesus monkey theta defensin anti-  
 CC viral peptide, which is given in the exemplification of the present  
 CC invention  
 CC  
 SQ Sequence 18 AA;  
 Query Match 87.0%; Score 100; DB 5; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 0.00071;  
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GICRCICTRGFCRCICGR 18  
 DB 1 GICRCICRGVCRCICGR 18  
 RESULT 14  
 AAE33864  
 ID AAE33864 standard; peptide; 18 AA.  
 AC AAE33864;  
 XX  
 XX 16-APR-2003 (first entry)  
 DT  
 XX Enantio-RC-101 retrocyclin peptide analogue.  
 XX  
 XX Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV;  
 KW human immunodeficiency virus; bacterial vaginosis; ophthalmic infection;



XX 16-APR-2003 (first entry)  
 DT Human retrocyclin peptide.  
 XX  
 XX Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV;  
 KW human immunodeficiency virus; bacterial vaginosis; ophthalmic infection;  
 KW antibiotic modelling; antimicrobial; human; cyclic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 1 /note= "Linked to amino acid at position 18 to form a  
 FT cyclic structure"  
 FT Disulfide-bond 3..16  
 FT Disulfide-bond 5..14  
 FT Disulfide-bond 7..12  
 FT Misc-difference 18 /note= "Linked to amino acid at position 1 to form a  
 FT cyclic structure"  
 FT  
 XX WO200285401-A1.  
 PN  
 XX 31-OCT-2002.  
 PD  
 XX 18-APR-2002; 2002WO-US012353.  
 XX  
 XX 18-APR-2001; 2001US-0284855P.  
 XX  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 XX  
 XX Lehrer RI, Waring AJ, Cole AM, Hong TB;  
 PI WPI; 2003-103387/09.  
 DR  
 XX  
 XX New isolated retrocyclin peptide, useful for preventing retroviral  
 PT infections in cells susceptible to bacterial or viral infections or  
 PT treating patients having the infections, such as HIV, sexually  
 PT transmitted diseases, vaginosis.  
 PT  
 XX  
 XX Claim 9; Page 24; 72pp; English.  
 PS  
 XX  
 XX The invention relates to novel retrocyclin peptides. Peptides and methods  
 CC of the invention are useful for preventing retroviral infections in cells  
 CC susceptible to bacterial or viral infections, or treating patients having  
 CC infections such as HIV (human immunodeficiency virus), sexually  
 CC transmitted diseases, bacterial vaginosis or ophthalmic infections. The  
 CC retrocyclin-mediated killing is useful for modelling and screening novel  
 CC antibiotic. The invention is also useful in gene therapy. The present  
 CC sequence is human retrocyclin peptide  
 CC  
 XX  
 SQ Sequence 18 AA;  
 SQ  
 XX  
 XX Query Match 88.7%; Score 102; DB 6; Length 18;  
 XX Best Local Similarity 88.9%; Pred. No. 0.00044;  
 XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GICRCICTRGFCRCICGR 18  
 DB 1 GICRCICGRCICRCICGR 18  
 DB  
 XX  
 XX RESULT 11  
 XX AAE33863  
 ID AAE33863 standard; peptide; 18 AA.  
 AC  
 XX AAE33863;  
 AC  
 XX 16-APR-2003 (first entry)  
 DT  
 XX Enantio-retrocyclin peptide analogue.  
 DE  
 XX

KW Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV;  
 KW human immunodeficiency virus; bacterial vaginosis; ophthalmic infection;  
 KW antibiotic modelling; antimicrobial; cyclic.  
 XX  
 XX Unidentified.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 1..18 /note= "D-form residues"  
 FT  
 FT Misc-difference 1 /note= "Linked to amino acid at position 18 to form a  
 FT cyclic structure"  
 FT Disulfide-bond 3..16  
 FT Disulfide-bond 5..14  
 FT Disulfide-bond 7..12  
 FT Misc-difference 18 /note= "Linked to amino acid at position 1 to form a  
 FT cyclic structure"  
 FT  
 XX WO200285401-A1.  
 PN  
 XX 31-OCT-2002.  
 PD  
 XX 18-APR-2002; 2002WO-US012353.  
 XX  
 XX 18-APR-2001; 2001US-0284855P.  
 XX  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 XX  
 XX Lehrer RI, Waring AJ, Cole AM, Hong TB;  
 PI WPI; 2003-103387/09.  
 DR  
 XX  
 XX New isolated retrocyclin peptide, useful for preventing retroviral  
 PT infections in cells susceptible to bacterial or viral infections or  
 PT treating patients having the infections, such as HIV, sexually  
 PT transmitted diseases, vaginosis.  
 PT  
 XX  
 XX Disclosure; Page 24; 72pp; English.  
 PS  
 XX  
 XX The invention relates to novel retrocyclin peptides. Peptides and methods  
 CC of the invention are useful for preventing retroviral infections in cells  
 CC susceptible to bacterial or viral infections, or treating patients having  
 CC infections such as HIV (human immunodeficiency virus), sexually  
 CC transmitted diseases, bacterial vaginosis or ophthalmic infections. The  
 CC retrocyclin-mediated killing is useful for modelling and screening novel  
 CC antibiotic. The invention is also useful in gene therapy. The present  
 CC sequence is human retrocyclin peptide analogue  
 CC  
 XX  
 SQ Sequence 18 AA;  
 SQ  
 XX  
 XX Query Match 88.7%; Score 102; DB 6; Length 18;  
 XX Best Local Similarity 88.9%; Pred. No. 0.00044;  
 XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GICRCICTRGFCRCICGR 18  
 DB 1 GICRCICGRCICRCICGR 18  
 DB  
 XX  
 XX RESULT 12  
 XX ADN08176  
 ID ADN08176 standard; peptide; 18 AA.  
 AC  
 XX ADN08176;  
 AC  
 XX 15-JUL-2004 (first entry)  
 DT  
 XX Human retrocyclin peptide, RC-100.  
 DE  
 XX retrocyclin; cyclic; primate; retroviral infection;  
 KW circular minidefensin; antibacterial; virucide; vaccine; immunotherapy;  
 KW microbial; viral; human.  
 KW

KM Monkey, Rheus theta defensin; RTD-2; antimicrobial peptide; cyclic;  
 KM anticubical; antiinflammatory; antibacterial; virucide; fungicide;  
 KM food; contact lens solution; eye wash solution; inflammatory response;  
 KM microbicidal inhibition; microbistatic growth inhibition; disinfectant;  
 KM food preservative; bacterial infection; viral infection;  
 KM fungal infection; haemolytic activity.  
 OS Macaca mulatta.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT 1. .18 /note="The peptide is cyclised by a covalent link  
 FT between these two residues"  
 FT Disulfide-bond 3. .16  
 FT Disulfide-bond 5. .14  
 FT Disulfide-bond 7. .12  
 XX  
 XX US2004014669-A1.  
 PN 22-JAN-2004.  
 PD 30-APR-2003; 2003US-00427715.  
 PF 30-APR-2002; 2002US-0377071P.  
 PR (REGC ) UNIV CALIFORNIA.  
 PA Selected ME, Tran DQ;  
 PI WPI; 2004-167945/16.  
 XX  
 DR Novel theta defensin analog useful for reducing or inhibiting growth or  
 XX survival of a microorganism in an environment such as food or food  
 PT product, contact lens solution, or eye wash solution, an inanimate  
 PT object.  
 PT  
 XX Example 1; SEQ ID NO 2; 46pp; English.  
 XX  
 XX The invention relates to a theta defensin analogue defined by formulae  
 CC detailed in the claims or appearing as ADO35239-ADO35257. The theta  
 CC defensin analogue is useful for reducing or inhibiting growth or survival  
 CC of a microorganism in an environment capable of sustaining the growth or  
 CC survival of the microorganism and is useful for reducing or inhibiting  
 CC growth or survival of a microorganism in an environment such as food or  
 CC food product, a solution (e.g., contact lens solution, or eye wash  
 CC solution), an inanimate object comprising surface, or a mammal. The  
 CC peptides are also useful for decreasing inflammatory response and for  
 CC microbicidal inhibition of survival of microorganism as well as  
 CC microbistatic inhibition of growth. Thus the peptides are useful as  
 CC therapeutic agents, disinfectants, food preservatives, or medicaments.  
 CC The peptides are also useful for treating a patient suffering from  
 CC bacterial, viral, fungal or other infection. The theta defensins have  
 CC high antimicrobial activity and low haemolytic activity. The present  
 CC sequence represents the rheus monkey wild-type theta defensin RTD-2.  
 CC  
 XX SQ Sequence 18 AA;  
 XX  
 XX  
 OY Query Match 89.6%; Score 103; DB 8; Length 18;  
 XX Best Local Similarity 88.9%; Pred. No. 0.00055;  
 XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 DB 1 GICRCICTRGFCRCICGR 18  
 1 GFCRCICTRGFCRCICTR 18  
 XX  
 RESULT 9  
 ABP53294  
 ID ABP53294 standard; peptide; 18 AA.  
 AC ABP53294;  
 XX  
 XX 13-NOV-2002 (first entry)

XX  
 XX Synthetic anti-viral human theta defensin peptide HTD-1 SEQ ID NO:27.  
 DE Anti-viral; viral infection; theta-defensin; lipid environment;  
 XX amphipathic alpha-helical structure; virucide; anti-HIV; immunisation;  
 KM viral growth inhibitor; viral proliferation inhibitor.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.  
 OS  
 PN MO200260468-A2.  
 XX  
 XX 08-AUG-2002.  
 PD 29-JAN-2002; 2002WO-US002435.  
 PF 30-JAN-2001; 2001US-0265270P.  
 PR 01-AUG-2001; 2001US-0309368P.  
 XX  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA Maury W, Stapleton J, Stinski M, Roller R, McCreary PB, Tack B;  
 XX WPI; 2002-674815/72.  
 XX  
 DR New method of using a first anti-viral peptide comprising a Theta-  
 PT defensin peptide in an amphipathic Alpha-helical structure in a lipid  
 PT environment for reducing the infectivity of a virus.  
 PT  
 XX Disclosure; Page 9; 65pp; English.  
 PS  
 XX The present invention describes a method (M1) of using a first anti-viral  
 CC peptide (I) comprising a theta-defensin peptide in an amphipathic alpha-  
 CC helical structure in a lipid environment for reducing the infectivity of  
 CC a virus. (I) can have virucide and anti-HIV activities, and can be used  
 CC to reduce virus growth, infectivity burden, shed, and development of anti-  
 CC -viral resistance. (I) can be used for inhibiting the growth and  
 CC proliferation of a virus and so can be used for: (a) protecting or  
 CC treating subject from a viral infection, preventing recurrent viral  
 CC infection in a subject harbouring a latent virus, controlling viral  
 CC spread within a virally-infected subject (VS), reducing viral burden in a  
 CC VS, reducing virus shed from a VS, reducing percentage of VS in a  
 CC population regardless of viral infection status, or inducing latency in a  
 CC VS; (b) reducing the infectivity of a virus; and (c) rendering virus-  
 CC contaminated tissue or fluid sample safe for use, or reducing the number  
 CC of infectious virus particles in a population of viruses. (M1) is useful  
 CC for reducing the infectivity of a virus in sheep, cattle, horses, swine,  
 CC cats, fowl and humans e.g. an enveloped virus infecting humans such as  
 CC human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is  
 CC administered to a patient who is immunosuppressed or to a subject who is  
 CC not infected with the virus, where the first anti-viral peptide is  
 CC administered prior to or subsequent to the virus contacting the subject.  
 CC The anti-viral peptide is most preferably administered to a subject who  
 CC is chronically, latently or acutely infected with the virus. The present  
 CC sequence represents a human theta defensin anti-viral peptide, which is  
 CC given in the exemplification of the present invention  
 XX  
 XX SQ Sequence 18 AA;  
 XX  
 XX  
 OY Query Match 88.7%; Score 102; DB 5; Length 18;  
 XX Best Local Similarity 88.9%; Pred. No. 0.00044;  
 XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 DB 1 GICRCICTRGFCRCICGR 18  
 1 GICRCICGRGICRCICGR 18  
 XX  
 RESULT 10  
 AAE33801  
 ID AAE33801 standard; peptide; 18 AA.  
 AC AAE33801;  
 XX

SQ Sequence 18 AA;

Query Match 90.4%; Score 104; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.00027;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GICRCICTRGFCRCIC 16  
| | | | | | | | | | | | | | | | | |  
DB 1 GICRCICTRGFCRCIC 16

RESULT 6

AAB35046  
ID AAB35046 standard; peptide; 18 AA.

AC AAB35046;

DT 27-MAR-2001 (first entry)

DE Theta defensin SEQ ID NO: 30.

XX Theta defensin; antimicrobial; cyclic; bacterium; fungus; protozoan;  
KW virus; helminth; disinfectant; food preservative; analogue.  
XX

OS Unidentified.

PN WO200068265-A1.

PD 16-NOV-2000.

PF 10-MAY-2000; 2000WO-US012842.

PR 10-MAY-1999; 99US-00309487.

PA (REGC ) UNIV CALIFORNIA.

PI Selected ME, Tang Y, Yuan J, Quellette AJ;

DR WPI, 2001-031853/04.

XX Novel theta defensin peptide with antimicrobial activity against  
PT bacteria, yeast, fungi, protozoa and viruses.  
XX

PS Claim 15; Fig 16; 110pp; English.

CC The present invention provides theta defensin peptides and analogues  
CC which have antimicrobial activity. They can be used in the treatment of  
CC bacterial, viral, fungal, protozoan and helminthic infections, in  
CC disinfectants and as food preservatives  
XX

SQ Sequence 18 AA;

Query Match 89.6%; Score 103; DB 4; Length 18;  
Best Local Similarity 88.9%; Pred. No. 0.00035;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GICRCICTRGFCRCICR 18  
| | | | | | | | | | | | | | | | | |  
DB 1 GFCRCICTRGFCRCICR 18

RESULT 7

AAB353295  
ID AAB353295 standard; peptide; 18 AA.

AC AAB353295;

DT 13-NOV-2002 (first entry)

DE Anti-viral theta defensin peptide RTD-2 SEQ ID NO:28.

XX Anti-viral; viral infection; theta-defensin; lipid environment;  
KW amphipathic alpha-helical structure; virucide; anti-HIV; immunisation;  
XX

KW viral growth inhibitor; viral proliferation inhibitor.

OS Maccaca mulatta.  
XX Synthetic.  
XX

PN WO200260468-A2.

PD 08-AUG-2002.

PF 29-JAN-2002; 2002WO-US002435.

PR 30-JAN-2001; 2001US-0265270P.

PR 01-AUG-2001; 2001US-0309368P.

PA (IOWA ) UNIV IOWA RES FOUNO.

DR WPI, 2002-674815/72.

DE New method of using a first anti-viral peptide comprising a Theta-

PT defensin peptide in an amphipathic Alpha-helical structure in a lipid  
PT environment for reducing the infectivity of a virus.  
XX

PS Disclosure; Page 10; 65pp; English.

CC The present invention describes a method (M1) of using a first anti-viral  
CC peptide (I) comprising a theta-defensin peptide in an amphipathic alpha-  
CC helical structure in a lipid environment for reducing the infectivity of  
CC a virus. (I) can have virucide and anti-HIV activities, and can be used  
CC to reduce virus growth, infectivity burden, shed, and development of anti-  
CC viral resistance. (I) can be used for inhibiting the growth and  
CC proliferation of a virus and so can be used for: (a) protecting or  
CC treating subject from a viral infection, preventing recurrent viral  
CC infection in a subject harbouring a latent virus, controlling viral  
CC spread within a virally-infected subject (VS), reducing viral burden in a  
CC VS, reducing virus shed from a VS, reducing percentage of VS in a  
CC population regardless of viral infection status, or inducing latency in a  
CC VS; (b) reducing the infectivity of a virus; and (c) rendering virus-  
CC contaminated tissue or fluid sample safe for use, or reducing the number  
CC of infectious virus particles in a population of viruses. (M1) is useful  
CC for reducing the infectivity of a virus in sheep, cattle, horses, swine,  
CC cats, fowl and humans e.g. an enveloped virus infecting humans such as  
CC human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is  
CC administered to a patient who is immunosuppressed or to a subject who is  
CC not infected with the virus, where the first anti-viral peptide is  
CC administered prior to or subsequent to the virus contacting the subject.  
CC The anti-viral peptide is most preferably administered to a subject who  
CC is chronically, latently or acutely infected with the virus. The present  
CC sequence represents a rhesus monkey theta defensin anti-viral peptide,  
CC which is given in the exemplification of the present invention  
XX

SQ Sequence 18 AA;

Query Match 89.6%; Score 103; DB 5; Length 18;  
Best Local Similarity 88.9%; Pred. No. 0.00035;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GICRCICTRGFCRCICR 18  
| | | | | | | | | | | | | | | | | |  
DB 1 GFCRCICTRGFCRCICR 18

RESULT 8

AD035230  
ID AD035230 standard; peptide; 18 AA.

AC AD035230;

DT 15-JUL-2004 (first entry)

DE Rhesus theta defensin peptide, RTD-2.

XX

infection, and a method for administering retrocyclin as a prophylactic agent to prevent a microbial or viral infection in a patient at risk of developing such infection. The retrocyclin peptide has antibacterial and virucide activities. The retrocyclin peptide can be used to treat a viral infection such as HIV-1. The retrocyclin peptide can be used as a vaccine and can be used in immunotherapy. The peptide and polypeptides are useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections. This sequence represents a retrocyclin peptide of the invention.

Sequence 18 AA;

Query Match 91.3%; Score 105; DB 8; Length 18;  
Best Local Similarity 88.9%; Pred. No. 0.00022;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GICRCITRGFCRCICGR 18  
Db 1 GICRCITRGFCRCICGR 18

RESULT 4  
AAE33866  
ID AAE33866 standard; peptide; 18 AA.

AAE33866;  
16-APR-2003 (first entry)

Macaca mulatta RTD1 peptide.

Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; rhesus monkey; theta defensin 1A; RTD1.

Macaca mulatta.

WO200285401-A1.

31-OCT-2002.

18-APR-2002; 2002WO-US012353.

18-APR-2001; 2001US-0284855P.

(REGC ) UNIV CALIFORNIA.

Lehrer RI, Waring AJ, Cole AM, Hong TB;

WPI; 2003-103387/09.

New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.

Example 1; Fig 3C; 72pp; English.

The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is rhesus monkey theta defensin, RTD1 peptide. This sequence is used in the exemplification of the invention

Sequence 18 AA;

Query Match 90.4%; Score 104; DB 6; Length 18;  
Best Local Similarity 83.3%; Pred. No. 0.00027;

Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GICRCITRGFCRCICGR 18  
Db 1 GICRCITRGFCRCICGR 18

RESULT 5  
AD035255  
ID AD035255 standard; peptide; 18 AA.

AD035255;

15-JUL-2004 (first entry)

Rhesus theta defensin analogue peptide RTD-4.

Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial; antiinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; fungal infection; haemolytic activity; cyclic.

Macaca mulatta.  
Synthetic.

Key Location/Qualifiers

Modified-site 1..18  
/note="The peptide is cyclised by a covalent link between these two residues"

Disulfide-bond 3..16  
Disulfide-bond 5..14  
Disulfide-bond 7..12

US2004014669-A1.

22-JAN-2004.

30-APR-2003; 2003US-00427715.

30-APR-2002; 2002US-0377071P.

(REGC ) UNIV CALIFORNIA.

Selected ME, Tran DQ;

WPI; 2004-167945/16.

Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate object.

Claim 1; SEQ ID NO 29; 46pp; English.

The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD035239-AD035257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.

CC spread within a virally-infected subject (VS), reducing viral burden in a  
CC VS, reducing virus shed from a VS, reducing percentage of VS in a  
CC population regardless of viral infection status, or inducing latency in a  
CC VS; (b) reducing the infectivity of a virus; and (c) rendering virus-  
CC contaminated tissue or fluid sample safe for use, or reducing the number  
CC of infectious virus particles in a population of viruses. (MI) is useful  
CC for reducing the infectivity of a virus in sheep, cattle, horses, swine,  
CC cats, fowl and humans e.g. an enveloped virus infecting humans such as  
CC human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is  
CC administered to a patient who is immunosuppressed or to a subject who is  
CC not infected with the virus, where the first anti-viral peptide is  
CC administered prior to or subsequent to the virus contacting the subject.  
CC The anti-viral peptide is most preferably administered to a subject who  
CC is chronically, latently or acutely infected with the virus. The present  
CC sequence represents a chimeric human/rhesus monkey theta defensin anti-  
CC viral peptide, which is given in the exemplification of the present  
CC invention

SO Sequence 18 AA;

Query Match 100.0%; Score 115; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GICRCICRGFCRCICGR 18  
DB 1 GICRCICRGFCRCICGR 18

RESULT 2

AAE33806  
ID AAE33806 standard; peptide; 18 AA.

AC AAE33806;

DT 16-APR-2003 (first entry)

XX 111Y retrocyclin peptide analogue.

DE Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV;

KW human immunodeficiency virus; bacterial vaginosis; ophthalmic infection;

KW antibiotic modelling; antimicrobial; cyclic.

OS Unidentified.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "linked to amino acid at position 18 to form a

FT cyclic structure"

FT Disulfide-bond 3..16  
FT Disulfide-bond 5..14  
FT Disulfide-bond 7..12  
FT Misc-difference 18 /note= "linked to amino acid at position 1 to form a

FT cyclic structure"

XX WO200285401-A1.

PD 31-OCT-2002.

XX 18-APR-2002; 2002WO-US012353.

PR 18-APR-2001; 2001US-0284855P.

XX (REGC ) UNIV CALIFORNIA.

PI Lehrer RI, Waring AJ, Cole AM, Hong TB;

XX WPI; 2003-103387/09.

PT New isolated retrocyclin peptide, useful for preventing retroviral  
PT infections in cells susceptible to bacterial or viral infections or  
PT treating patients having the infections, such as HIV, sexually

PT transmitted diseases, vaginosis.  
XX  
PS Claim 9; Page 24; 72pp; English.

CC The invention relates to novel retrocyclin peptides. Peptides and methods  
CC of the invention are useful for preventing retroviral infections in cells  
CC susceptible to bacterial or viral infections, or treating patients having  
CC infections such as HIV (human immunodeficiency virus), sexually  
CC transmitted diseases, bacterial vaginosis or ophthalmic infections. The  
CC retrocyclin-mediated killing is useful for modelling and screening novel  
CC antibiotics. The invention is also useful in gene therapy. The present  
CC sequence is human retrocyclin peptide analogue

SO Sequence 18 AA;

Query Match 91.3%; Score 105; DB 6; Length 18;  
Best Local Similarity 88.9%; Pred. No. 0.00022;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GICRCICRGFCRCICGR 18  
DB 1 GICRCICRGFCRCICGR 18

RESULT 3

ADN08181  
ID ADN08181 standard; peptide; 18 AA.

AC ADN08181;

DT 15-JUL-2004 (first entry)

XX Human retrocyclin peptide, RC-105.

DE retrocyclin; cyclic; primate; retroviral infection;

KW circular miniddefensin; antibacterial; virucide; vaccine; immunotherapy;

KW microbial; viral; human.

XX Homo sapiens.

OS Synthetic.

XX WO2004033479-A2.

PD 22-APR-2004.

XX 06-MAY-2003; 2003WO-US014106.

PR 06-MAY-2002; 2002US-00141645.

XX (REGC ) UNIV CALIFORNIA.

PI (LEHRER) LEHRER R I.  
PA (WARI) WARING A J.  
PA (COLE) COLE A M.  
PA (HONG) HONG T B.

PI Lehrer RI, Waring AJ, Cole AM, Hong TB;

XX WPI; 2004-340883/31.

PT New isolated retrocyclin peptides and cyclic polypeptides, useful as  
PT therapeutic and prophylactic agents for treating and preventing microbial  
PT and viral infections.

PS Claim 9; SEQ ID NO 6; 82pp; English.

CC The invention relates to a novel isolated retrocyclin peptide. The  
CC invention further provides: a cyclic polypeptide; an isolated nucleic  
CC acid encoding a primate retrocyclin; a method for preventing retroviral  
CC infection in a cell by administering an effective dose of a circular  
CC miniddefensin or retrocyclin to the cell; a method for killing microbial  
CC organisms by administering an effective dose of retrocyclin to the  
CC microbial organisms; a method for administering retrocyclin as a  
CC therapeutic agent to a patient with an established microbial or viral

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# OM protein - protein search, using sw model

Run on: March 22, 2005, 20:22:01 ; Search time 164 Seconds  
(without alignments)  
42.449 Million cell updates/sec

Title: US-10-721-839-32

Perfect score: 115  
Sequence: 1 GICRCITRGFCRCICGR 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1808:\*
- 2: geneseqp1908:\*
- 3: geneseqp2000:\*
- 4: geneseqp2001:\*
- 5: geneseqp2002:\*
- 6: geneseqp2003:\*
- 7: geneseqp2003b:\*
- 8: geneseqp2004:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	18	5	ABP53299 Anti-vira
2	105	91.3	18	6	AAE33806 IL1Y retr
3	105	91.3	18	8	ADN08181 Human ret
4	104	90.4	18	6	AAE33866 Macaca mu
5	104	90.4	18	8	AD035255 Rhesus th
6	103	89.6	18	4	AAE35046 Theta def
7	103	89.6	18	5	ABP53295 Anti-vira
8	103	89.6	18	5	ABP53294 Synthetic
9	102	88.7	18	5	ABP53294 Synthetic
10	102	88.7	18	6	AAE33801 Human ret
11	102	88.7	18	6	AAE33863 Enanti-o-r
12	102	88.7	18	8	ADN08178 Human ret
13	100	87.0	18	5	ABP53298 Anti-vira
14	99	86.1	18	6	AAE33864 Enanti-o-R
15	99	86.1	18	6	AAE33802 R9K retro
16	99	86.1	18	8	ADN08177 Human ret
17	98	85.2	18	8	AD035240 Rhesus th
18	97	84.3	18	6	AAE33805 IL1Y retr
19	97	84.3	18	6	AAE33804 IL1Y retr
20	97	84.3	18	6	AAE33803 IL1Y retr
21	97	84.3	18	8	ADN08179 Human ret
22	97	84.3	18	8	ADN08180 Human ret
23	97	84.3	18	8	ADN08178 Human ret
24	95	82.6	18	6	AAE33807 R9Y retro
25	95	82.6	18	8	ADN08182 Human ret

26	94	81.7	18	6	AAE33865 RC-101/10
27	93.5	81.3	18	8	AD035263 Monkey RT
28	89	77.4	18	4	AAE35047 Theta def
29	89	77.4	18	5	ABP53296 Anti-vira
30	89	77.4	18	8	AAE33810 Retrocycl
31	89	77.4	18	8	AD035242 Rhesus th
32	89	77.4	18	8	AD035241 Rhesus th
33	89	77.4	18	8	AD035241 Rhesus th
34	89	77.4	18	8	AD035256 Rhesus th
35	88	76.5	18	4	AAE35030 Theta def
36	88	76.5	18	5	ABP53297 Anti-vira
37	88	76.5	18	7	AD095202 Cyclic de
38	88	76.5	18	8	AD035357 Antimicro
39	88	76.5	18	8	AD070012 Rhesus th
40	88	76.5	18	8	AD035229 Rhesus th
41	88	76.5	18	8	AD035238 Rhesus th
42	88	76.5	18	8	AD035239 Rhesus th
43	88	76.5	18	8	AD035250 Rhesus th
44	87	75.7	18	6	AAE33809 R13Y retr
45	87	75.7	18	6	AAE33808 R9Y retro

## ALIGNMENTS

RESULT 1  
ID ABE53299 standard; peptide; 18 AA.  
XX  
AC ABE53299;  
XX  
DT 13-NOV-2002 (first entry)  
DE Anti-viral chimeric theta defensin peptide H/RTD-2 SEQ ID NO.32.  
XX  
KW Anti-viral; viral infection; theta-defensin; lipid environment;  
XX amphipathic alpha-helical structure; virucide; anti-HIV; immunisation;  
XX viral growth inhibitor; viral proliferation inhibitor.  
XX  
OS Homo sapiens.  
OS Macaca mulatta.  
OS Synthetic.  
XX  
PN WO200260468-A2.  
XX  
PD 08-AUG-2002.  
XX  
PF 29-JAN-2002; 2002WO-US002435.  
XX  
PR 30-JAN-2001; 2001US-0265270P.  
PR 01-AUG-2001; 2001US-0309368P.  
XX  
PA (IOWA ) UNIV IOWA RES FOUND.  
XX  
PI Maury W, Stapleton J, Stinski M, Roller R, Mccray PB, Tack B;  
XX  
DR WPI; 2002-674815/72.  
XX  
PT New method of using a first anti-viral peptide comprising a Theta-  
PT defensin peptide in an amphipathic Alpha-helical structure in a lipid  
PT environment for reducing the infectivity of a virus.  
XX  
PS Disclosure; Page 10; 65pp; English.  
XX  
CC The present invention describes a method (M1) of using a first anti-viral  
CC peptide (I) comprising a theta-defensin peptide in an amphipathic alpha-  
CC helical structure in a lipid environment for reducing the infectivity of  
CC a virus. (I) can have virucide and anti-HIV activities, and can be used  
CC to reduce virus growth, infectivity burden, shed, and development of anti-  
CC viral resistance. (I) can be used for inhibiting the growth and  
CC proliferation of a virus and so can be used for: (a) protecting or  
CC treating subject from a viral infection, preventing recurrent viral  
CC infection in a subject harbouring a latent virus, controlling virus

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OM protein - protein search, using sw model

Run on: March 22, 2005, 20:46:53 ; Search time 141 Seconds  
(without alignments)  
42.197 Million cell updates/sec

Title: US-10-721-839-32

Perfect score: 115

Sequence: 1 GICRCICTRGFCRCICGR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1401741 seqs, 330541175 residues

Total number of hits satisfying chosen parameters: 1401741

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/2/pubppaa/PCRT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubppaa/PCRTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pep:\*  
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10: /cgn2\_6/ptodata/2/pubppaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubppaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubppaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubppaa/US10E\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubppaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	18	14	US-10-060-102-32
2	115	100.0	18	15	US-10-721-839-32
3	105	91.3	18	14	US-10-141-645-6
4	104	90.4	18	15	US-10-427-715-29
5	103	89.6	18	14	US-10-060-102-28
6	103	89.6	18	15	US-10-427-715-2
7	103	89.6	18	15	US-10-427-715-14
8	103	89.6	18	15	US-10-721-839-28
9	102	88.7	18	14	US-10-060-102-27
10	102	88.7	18	14	US-10-141-645-1
11	102	88.7	18	15	US-10-721-839-27
12	100	87.0	18	14	US-10-060-102-31
13	100	87.0	18	15	US-10-721-839-31

14	99	86.1	18	14	US-10-141-645-2	Sequence 2, Appl1
15	97	84.3	18	14	US-10-141-645-3	Sequence 3, Appl1
16	97	84.3	18	14	US-10-141-645-4	Sequence 4, Appl1
17	97	84.3	18	14	US-10-141-645-5	Sequence 5, Appl1
18	95	82.6	18	14	US-10-141-645-7	Sequence 7, Appl1
19	89	77.4	18	14	US-10-060-102-29	Sequence 29, Appl1
20	89	77.4	18	15	US-10-427-715-3	Sequence 3, Appl1
21	89	77.4	18	15	US-10-427-715-15	Sequence 15, Appl1
22	89	77.4	18	15	US-10-427-715-16	Sequence 16, Appl1
23	89	77.4	18	15	US-10-427-715-30	Sequence 30, Appl1
24	89	77.4	18	15	US-10-721-839-29	Sequence 29, Appl1
25	88	76.5	18	14	US-10-060-102-30	Sequence 30, Appl1
26	88	76.5	18	14	US-10-313-994-1	Sequence 1, Appl1
27	88	76.5	18	15	US-10-427-715-1	Sequence 12, Appl1
28	88	76.5	18	15	US-10-427-715-12	Sequence 13, Appl1
29	88	76.5	18	15	US-10-427-715-13	Sequence 24, Appl1
30	88	76.5	18	15	US-10-427-715-24	Sequence 30, Appl1
31	88	76.5	18	15	US-10-721-839-30	Sequence 8, Appl1
32	87	75.7	18	14	US-10-141-645-8	Sequence 9, Appl1
33	87	75.7	18	14	US-10-141-645-9	Sequence 53, Appl1
34	86	74.8	18	9	US-09-917-340-53	Sequence 17, Appl1
35	86	74.8	18	15	US-10-427-715-17	Sequence 31, Appl1
36	86	74.8	18	15	US-10-427-715-31	Sequence 53, Appl1
37	86	74.8	18	17	US-10-844-837-53	Sequence 9, Appl1
38	85	73.9	18	14	US-10-313-994-9	Sequence 28, Appl1
39	77	67.0	18	15	US-10-427-715-28	Sequence 21, Appl1
40	76	66.1	18	15	US-10-427-715-23	Sequence 51, Appl1
41	73	63.5	92	14	US-10-313-994-21	Sequence 37, Appl1
42	72	62.6	101	11	US-09-833-245-511	Sequence 38, Appl1
43	71	61.7	18	15	US-10-427-715-38	Sequence 39, Appl1
44	71	61.7	18	15	US-10-427-715-39	
45	71	61.7	18	15	US-10-427-715-39	

## ALIGNMENTS

RESULT 1

US-10-060-102-32

Sequence 32, Application US/10060102

Publication No. US20030022829A1

GENERAL INFORMATION:

APPLICANT: MAURY, WENDY

APPLICANT: STAPLETON, JACK

APPLICANT: ROLLER, RICHARD

APPLICANT: STINSKI, MARK

APPLICANT: MCCRAY, PAUL B.

TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIA

TITLE OF INVENTION: CATHELICIDINS

FILE REFERENCE: IOWA.035US

CURRENT APPLICATION NUMBER: US/10/060.102

PRIOR FILING DATE: 2002-02-22

PRIOR APPLICATION NUMBER: 60/309,368

PRIOR FILING DATE: 2001-08-01

PRIOR APPLICATION NUMBER: 60/265,270

PRIOR FILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 32

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptide

US-10-060-102-32

Query Match 100.0%; Score 115; DB 14; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.8e-06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GICRCICTRGFCRCICGR 18

Db 1 GICRCICTRGFCRCICGR 18

## RESULT 2

US-10-721-839-32  
; Sequence 32, Application US/10721839  
; Publication No. US20040086535A1  
; GENERAL INFORMATION:  
; APPLICANT: MAURY, WENDY  
; APPLICANT: STRAPLETON, JACK  
; APPLICANT: ROLLER, RICHARD  
; APPLICANT: STINSKI, MARK  
; APPLICANT: MCCRAY, PAUL B.  
; APPLICANT: TACK, BRIAN  
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI  
; FILE REFERENCE: IOWA:035US  
; CURRENT APPLICATION NUMBER: US/10/721,839  
; CURRENT FILING DATE: 2003-11-25  
; PRIOR APPLICATION NUMBER: US/10/060,102  
; PRIOR FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 60/309,368  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/265,270  
; PRIOR FILING DATE: 2001-01-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-721-839-32

Query Match 100.0%; Score 115; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18  
Db 1 GICRCICTRGFCRCICGR 18

## RESULT 3

US-10-141-645-6  
; Sequence 6, Application US/10141645  
; Publication No. US20030144184A1  
; GENERAL INFORMATION:  
; APPLICANT: Robert Lehnner  
; APPLICANT: Alan Waring  
; APPLICANT: Alexander Cole  
; APPLICANT: Teresa Hong  
; TITLE OF INVENTION: Retrocyclins - Antiviral and  
; TITLE OF INVENTION: Antimicrobial Peptides  
; FILE REFERENCE: UCLA-001CIP  
; CURRENT APPLICATION NUMBER: US/10/141,645  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: 60/284,855  
; PRIOR FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: Unassigned  
; PRIOR FILING DATE: 2002-04-18  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic variant  
US-10-141-645-6

Query Match 91.3%; Score 105; DB 14; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.3e-05;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18  
Db 1 GICRCICTRGFCRCICGR 18

## RESULT 4

US-10-427-715-29  
; Sequence 29, Application US/10427715  
; Publication No. US20040014669A1  
; GENERAL INFORMATION:  
; APPLICANT: Tran, Dat Q.  
; APPLICANT: Seisted, Michael E.  
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs  
; TITLE OF INVENTION: Theroef, and Methods of Use  
; FILE REFERENCE: 66778-302(UC5754)  
; CURRENT APPLICATION NUMBER: US/10/427,715  
; CURRENT FILING DATE: 2003-04-30  
; PRIOR APPLICATION NUMBER: US 60/377,071  
; PRIOR FILING DATE: 2002-04-30  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic construct  
US-10-427-715-29

Query Match 90.4%; Score 104; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.9e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCIC 16  
Db 1 GICRCICTRGFCRCIC 16

## RESULT 5

US-10-060-102-28  
; Sequence 28, Application US/10060102  
; Publication No. US200300282829A1  
; GENERAL INFORMATION:  
; APPLICANT: MAURY, WENDY  
; APPLICANT: STRAPLETON, JACK  
; APPLICANT: ROLLER, RICHARD  
; APPLICANT: STINSKI, MARK  
; APPLICANT: MCCRAY, PAUL B.  
; APPLICANT: TACK, BRIAN  
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI  
; TITLE OF INVENTION: CATHELICIDINS  
; FILE REFERENCE: IOWA:035US  
; CURRENT APPLICATION NUMBER: US/10/060,102  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 60/309,368  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/265,270  
; PRIOR FILING DATE: 2001-01-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-060-102-28



Query Match 89.6%; Score 103; DB 14; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.8e-05;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GICRCICTRGRCRCICGR 18  
Db 1 GFCRCICTRGRCRCICTR 18

RESULT 6  
US-10-427-715-2

; Sequence 2, Application US/10427715  
; Publication No. US20040014669A1  
; GENERAL INFORMATION:  
; APPLICANT: Seasted, Michael E.  
; APPLICANT: Tran, Dat Q.  
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs  
; FILE REFERENCE: 66778-302(UC5754)  
; CURRENT APPLICATION NUMBER: US/10/427,715  
; CURRENT FILING DATE: 2003-04-30  
; PRIOR APPLICATION NUMBER: US 60/377,071  
; PRIOR FILING DATE: 2002-04-30  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Macaca mulatta  
US-10-427-715-2

Query Match 89.6%; Score 103; DB 15; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.8e-05;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GICRCICTRGRCRCICGR 18  
Db 1 GFCRCICTRGRCRCICTR 18

RESULT 7  
US-10-427-715-14

; Sequence 14, Application US/10427715  
; Publication No. US20040014669A1  
; GENERAL INFORMATION:  
; APPLICANT: Seasted, Michael E.  
; APPLICANT: Tran, Dat Q.  
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs  
; FILE REFERENCE: 66778-302(UC5754)  
; CURRENT APPLICATION NUMBER: US/10/427,715  
; CURRENT FILING DATE: 2003-04-30  
; PRIOR APPLICATION NUMBER: US 60/377,071  
; PRIOR FILING DATE: 2002-04-30  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic construct  
US-10-427-715-14

Query Match 89.6%; Score 103; DB 15; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.8e-05;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GICRCICTRGRCRCICGR 18  
Db 1 GFCRCICTRGRCRCICTR 18

RESULT 8  
US-10-721-839-28

; Sequence 28, Application US/10721839  
; Publication No. US20040086535A1  
; GENERAL INFORMATION:  
; APPLICANT: MAURY, WENDY  
; APPLICANT: STAPLETON, JACK  
; APPLICANT: ROLLER, RICHARD  
; APPLICANT: STINSKI, MARK  
; APPLICANT: MCCRAY, PAUL B.  
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIAN  
; FILE REFERENCE: IOWA:035US  
; CURRENT APPLICATION NUMBER: US/10/721,839  
; CURRENT FILING DATE: 2003-11-25  
; PRIOR APPLICATION NUMBER: US/10/060,102  
; PRIOR FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 60/309,368  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/265,270  
; PRIOR FILING DATE: 2001-01-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-721-839-28

Query Match 89.6%; Score 103; DB 15; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.8e-05;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GICRCICTRGRCRCICGR 18  
Db 1 GFCRCICTRGRCRCICTR 18

RESULT 9  
US-10-060-102-27

; Sequence 27, Application US/10060102  
; Publication No. US20030022829A1  
; GENERAL INFORMATION:  
; APPLICANT: MAURY, WENDY  
; APPLICANT: STAPLETON, JACK  
; APPLICANT: ROLLER, RICHARD  
; APPLICANT: STINSKI, MARK  
; APPLICANT: MCCRAY, PAUL B.  
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIAN  
; FILE REFERENCE: IOWA:035US  
; CURRENT APPLICATION NUMBER: US/10/060,102  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 60/309,368  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/265,270  
; PRIOR FILING DATE: 2001-01-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-060-102-27

Query Match 88.7%; Score 102; DB 14; Length 18;  
Best Local Similarity 88.9%; Pred. No. 4.9e-05;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18  
|||||  
DB 1 GICRCICGRGICRCICGR 18

RESULT 10  
US-10-141-645-1  
Sequence 1, Application US/10141645  
Publication No. US20030144184A1  
GENERAL INFORMATION:

APPLICANT: Robert Lehrer  
APPLICANT: Alan Marling  
APPLICANT: Alexander Cole  
APPLICANT: Teresa Hong  
TITLE OF INVENTION: Retrocyclins - Antiviral and  
TITLE OF INVENTION: Antimicrobial Peptides  
FILE REFERENCE: UCLA-001CIP  
CURRENT APPLICATION NUMBER: US/10/141,645  
CURRENT FILING DATE: 2002-05-06  
PRIOR APPLICATION NUMBER: 60/284,855  
PRIOR FILING DATE: 2001-04-18  
PRIOR APPLICATION NUMBER: Unassigned  
PRIOR FILING DATE: 2002-04-18  
NUMBER OF SEQ ID NOS: 125  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-141-645-1

Query Match 88.7%; Score 102; DB 14; Length 18;  
Best Local Similarity 88.9%; Pred. No. 4.9e-05;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18  
|||||  
DB 1 GICRCICGRGICRCICGR 18

RESULT 11  
US-10-721-839-27

Sequence 27, Application US/10721839  
Publication No. US20040086535A1  
GENERAL INFORMATION:  
APPLICANT: MAURY, WENDY  
APPLICANT: STAPLETON, JACK  
APPLICANT: ROLLER, RICHARD  
APPLICANT: STINSKI, MARK  
APPLICANT: MCCRAY, PAUL B.  
APPLICANT: TACK, BRIAN  
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI  
TITLE OF INVENTION: CATHELICIDINS  
FILE REFERENCE: IOWA:035US  
CURRENT APPLICATION NUMBER: US/10/721,839  
CURRENT FILING DATE: 2003-11-25  
PRIOR APPLICATION NUMBER: US/10/060,102  
PRIOR FILING DATE: 2002-02-22  
PRIOR APPLICATION NUMBER: 60/309,368  
PRIOR FILING DATE: 2001-08-01  
PRIOR APPLICATION NUMBER: 60/265,270  
PRIOR FILING DATE: 2001-01-30  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 27  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Peptide  
US-10-721-839-27

Query Match 88.7%; Score 102; DB 15; Length 18;  
Best Local Similarity 88.9%; Pred. No. 4.9e-05;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18  
|||||  
DB 1 GICRCICGRGICRCICGR 18

RESULT 12  
US-10-060-102-31

Sequence 31, Application US/10060102  
Publication No. US20030022829A1  
GENERAL INFORMATION:  
APPLICANT: MAURY, WENDY  
APPLICANT: STAPLETON, JACK  
APPLICANT: ROLLER, RICHARD  
APPLICANT: STINSKI, MARK  
APPLICANT: MCCRAY, PAUL B.  
APPLICANT: TACK, BRIAN  
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI  
TITLE OF INVENTION: CATHELICIDINS  
FILE REFERENCE: IOWA:035US  
CURRENT APPLICATION NUMBER: US/10/060,102  
CURRENT FILING DATE: 2002-02-22  
PRIOR APPLICATION NUMBER: 60/309,368  
PRIOR FILING DATE: 2001-08-01  
PRIOR APPLICATION NUMBER: 60/265,270  
PRIOR FILING DATE: 2001-01-30  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 31  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Peptide  
US-10-060-102-31

Query Match 87.0%; Score 100; DB 14; Length 18;  
Best Local Similarity 83.3%; Pred. No. 8.2e-05;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18  
|||||  
DB 1 GICRCICGRGICRCICGR 18

RESULT 13  
US-10-721-839-31

Sequence 31, Application US/10721839  
Publication No. US20040086535A1  
GENERAL INFORMATION:  
APPLICANT: MAURY, WENDY  
APPLICANT: STAPLETON, JACK  
APPLICANT: ROLLER, RICHARD  
APPLICANT: STINSKI, MARK  
APPLICANT: MCCRAY, PAUL B.  
APPLICANT: TACK, BRIAN  
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI  
TITLE OF INVENTION: CATHELICIDINS  
FILE REFERENCE: IOWA:035US  
CURRENT APPLICATION NUMBER: US/10/721,839  
CURRENT FILING DATE: 2003-11-25  
PRIOR APPLICATION NUMBER: US/10/060,102  
PRIOR FILING DATE: 2002-02-22  
PRIOR APPLICATION NUMBER: 60/309,368

;; PRIOR FILING DATE: 2001-08-01  
;; PRIOR APPLICATION NUMBER: 60/265,270  
;; PRIOR FILING DATE: 2001-01-30  
;; NUMBER OF SEQ ID NOS: 32  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 31  
;; LENGTH: 18  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: Peptide  
US-10-721-839-31

Query Match 87.0%; Score 100; DB 15; Length 18;  
Best Local Similarity 83.3%; Pred. No. 8.2e-05;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GICRCICTRGFCRCICGR 18  
|||:|||||  
Db 1 GICRCLCRGVCRICICGR 18

RESULT 14  
US-10-141-645-2  
; Sequence 2, Application US/10141645  
; Publication No. US20030144184A1  
; GENERAL INFORMATION:  
; APPLICANT: Robert Lehrer  
; APPLICANT: Alan Waring  
; APPLICANT: Alexander Cole  
; APPLICANT: Teresa Hong  
; TITLE OF INVENTION: Retrocyclins - Antiviral and  
; TITLE OF INVENTION: Antimicrobial Peptides  
; FILE REFERENCE: UCLA-001CIP  
; CURRENT APPLICATION NUMBER: US/10/141,645  
; PRIOR FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: 60/284,855  
; PRIOR FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: Unassigned  
; PRIOR FILING DATE: 2002-04-18  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic variant  
US-10-141-645-2

Query Match 86.1%; Score 99; DB 14; Length 18;  
Best Local Similarity 83.3%; Pred. No. 0.00011;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GICRCICTRGFCRCICGR 18  
|||:|||||  
Db 1 GICRCICGICRCICICGR 18

RESULT 15  
US-10-141-645-3  
; Sequence 3, Application US/10141645  
; Publication No. US20030144184A1  
; GENERAL INFORMATION:  
; APPLICANT: Robert Lehrer  
; APPLICANT: Alan Waring  
; APPLICANT: Alexander Cole  
; APPLICANT: Teresa Hong  
; TITLE OF INVENTION: Retrocyclins - Antiviral and  
; TITLE OF INVENTION: Antimicrobial Peptides  
; FILE REFERENCE: UCLA-001CIP  
; CURRENT APPLICATION NUMBER: US/10/141,645

;; CURRENT FILING DATE: 2002-05-06  
;; PRIOR APPLICATION NUMBER: 60/284,855  
;; PRIOR FILING DATE: 2001-04-18  
;; PRIOR APPLICATION NUMBER: Unassigned  
;; PRIOR FILING DATE: 2002-04-18  
;; NUMBER OF SEQ ID NOS: 125  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 3  
;; LENGTH: 18  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: synthetic variant  
US-10-141-645-3

Query Match 84.3%; Score 97; DB 14; Length 18;  
Best Local Similarity 83.3%; Pred. No. 0.00018;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GICRCICTRGFCRCICGR 18  
|||:|||||  
Db 1 GICRCICGICRCICICGR 18

Search completed: March 22, 2005, 21:02:08  
Job time : 144 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: March 22, 2005, 20:37:47 ; Search time 39 Seconds  
(without alignments)  
44,408 Million cell updates/sec

Title: US-10-721-839-32

Perfect score: 115

Sequence: 1 GICRCICTRGFCRCICGR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database: PIR 79:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	86	74.8	18	2	CS9089	theta defensin-1 -
2	64	55.7	76	2	A59089	theta defensin 1a
3	57.5	50.0	248	2	E71602	probable integral
4	51	44.3	164	2	T24272	hypothetical prote
5	51	44.3	188	2	T15651	hypothetical prote
6	51	44.3	306	2	S32814	methylviologen-red
7	50.5	43.9	3461	2	S58870	reelin precursor -
8	49.5	43.0	282	2	JC5677	RNA4 protein - Bee
9	49	42.6	72	1	T1MB	trypsin inhibitor
10	49	42.6	73	2	JC1066	trypsin inhibitor
11	49	42.6	1700	2	S08167	Balbani ring 3 pr
12	49	42.6	3191	2	T22945	hypothetical prote
13	48.5	42.2	83	2	S07405	proteinase inhibit
14	48.5	42.2	94	2	TJ5Y22	Bowman-Birk protei
15	48.5	42.2	103	1	JC5Y22	proteinase inhibit
16	48.5	42.2	419	2	S69207	vascular endotheli
17	48	41.7	152	2	T18975	hypothetical prote
18	48	41.7	157	2	A25964	thyroglobulin - ra
19	48	41.7	624	1	S54581	probable membrane
20	48	41.7	2946	2	T15840	hypothetical prote
21	47	40.9	78	1	T1ZB1P	proteinase inhibit
22	47	40.9	72	1	T1ZB1P	proteinase inhibit
23	47	40.9	113	2	S56648	trypsin inhibitor
24	47	40.9	195	2	T28803	hypothetical prote
25	47	40.9	290	2	G72858	AcOxT-70 protein -
26	47	40.9	1353	1	JH0675	restrictin precurs
27	47	40.9	1394	2	A35626	transforming growt
28	47	40.9	1733	1	B45344	probable nuclear a
29	47	40.9	1958	2	B40505	hypothetical prote

30	47	40.9	2195	2	T34264	hypothetical prote
31	46.5	40.4	95	2	S02186	hypothetical prote
32	46.5	40.4	143	2	B21761	high cysteine chor
33	46.5	40.4	1131	2	T15617	hypothetical prote
34	46.5	40.4	2871	2	A55567	fibrillin I - bov
35	46.5	40.4	2871	2	A55567	fibrillin I - bov
36	46.5	40.4	3002	2	A47221	fibrillin-1 precu
37	46	40.0	64	2	A25775	metallothionein A
38	46	40.0	64	2	A33825	metallothionein A
39	46	40.0	79	1	T1F82	proteinase inhibit
40	46	40.0	83	2	S07941	proteinase inhibit
41	46	40.0	102	1	T1SYD2	proteinase inhibit
42	46	40.0	146	2	S09415	proteinase inhibit
43	46	40.0	160	2	T25185	hypothetical prote
44	46	40.0	195	2	JH0719	omega-conotoxin re
45	46	40.0	276	2	F71262	hypothetical prote

## ALIGNMENTS

### RESULT 1

CS9089

theta defensin-1 - rhesus macaque

N:Alternate names: RTD-1

C:Species: Macaca mulatta (rhesus macaque)

C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999

C:Accession: CS9089

R:Tang, Y.Q.; Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J.;

Science 286, 498-502, 1999

A:Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation o

A:Reference number: A59089; MUID:99453140; PMID:10521339

A:Accession: CS9089

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 <SEL>

A>Note: this sequence is cyclically permuted by -6 residues from the sequence presented

C:Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing

F:1-9/Region: theta defensin 1a-derived

F:10-18/Region: theta defensin 1b-derived

F:1-18/Cross-link: cyclopeptide (Arg-Cys) #status experimental

F:2-11,4-9,13-18/Disulfide bonds: #status experimental

F:9-10/Cross-link: cyclopeptide (Cys-Arg) #status experimental

Query Match

Best Local Similarity 86.7%; Score 86; DB 2; Length 18;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RCICTRGFCRCICGR 18

DB 1 RCICTRGFCRCICGR 15

### RESULT 2

A59089

theta defensin 1a precursor - rhesus macaque

C:Species: Macaca mulatta (rhesus macaque)

C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

C:Accession: A59089

R:Tang, Y.Q.; Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J.;

Science 286, 498-502, 1999

A:Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation of

A:Reference number: A59089; MUID:99453140; PMID:10521339

A:Accession: A59089

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-76 <RNA>

A:Cross-references: UNIPROT:P82270; GB:AF191100; NID:66137227; PID:AA04389.1; PID:66137227

C:Comment: For the complete mature sequence, see PIR:A59089 and PIR:B59089.

C:Superfamily: mammalian defensin

C:Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-64/Domain: amino-terminal propeptide #status predicted <PRO>  
F:74-76/Domain: carboxyl-terminal propeptide #status predicted <CTR>

Query Match 55.7%; Score 64; DB 2; Length 76;  
Best Local Similarity 83.3%; Pred. No. 0.23;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RCICTRGFCRCI 15  
DB 65 RCICTRGFCRL 76

## RESULT 3

E71602  
probable integral membrane protein PFB0950W - malaria parasite (Plasmodium falciparum)

C/Species: Plasmodium falciparum  
C/Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 09-Jul-2004

C/Accession: E71602

R/Gardner, M.J.; Tectel, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;

Perera, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.

Science 282, 1126-1132, 1998

A/Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.

A/Reference number: A71600; MUID:99021743; PMID:9804551

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-248 <GAR>

A/Cross-references: UNIPROT:Q96282; GB:AE001428; GB:AE001362; NID:93845316; PIDN:AACT197

A/Experimental source: clone 3D7

C/Genetics:

A/Gene: PFB0950W

Query Match 50.0%; Score 57.5; DB 2; Length 248;  
Best Local Similarity 66.7%; Pred. No. 3;  
Matches 10; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY 2 ICRCICTRGFCRCIC 16  
DB 162 ICSCICT---CTCIC 173

## RESULT 4

T24272

hypothetical protein T01B7.8 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T24272

R/Stim, M.

submitted to the EMBL Data Library, October 1995

A/Reference number: Z19867

A/Accession: T24272

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: DNA

A/Residues: 1-164 <ML>

A/Cross-references: UNIPROT:Q20248; EMBL:Z66499; PIDN:CAA91301.1; GSPDB:GN00020; CESP:TC

A/Experimental source: clone T01B7

C/Genetics:

A/Gene: CESP:T01B7.8

A/Map position: 2

A/Introns: 20/3; 90/2

Query Match 44.3%; Score 51; DB 2; Length 164;  
Best Local Similarity 50.0%; Pred. No. 14;  
Matches 9; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18  
DB 80 GCGGCCCCRRPCCCCRR 97

## RESULT 5

T15651

hypothetical protein C27A2.5 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans  
C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C/Accession: T15651

R/Nhan, M.

submitted to the EMBL Data Library, May 1996

A/Description: The sequence of C. elegans cosmid C27A2.

A/Reference number: Z18382

A/Accession: T15651

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: DNA

A/Residues: 1-188 <NHA>

A/Cross-references: UNIPROT:Q18238; EMBL:U58760; NID:G1330384; PID:G1330389; PIDN:AA0077

A/Experimental source: strain Bristol NZ; clone C27A2

C/Genetics:

A/Gene: CESP:C27A2.5

A/Map position: 2

A/Introns: 19/3; 91/2

Query Match 44.3%; Score 51; DB 2; Length 188;  
Best Local Similarity 50.0%; Pred. No. 15;  
Matches 9; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18  
DB 81 GCGGCCCCRRPCCCCRR 98

## RESULT 6

S32834

methylviologen-reducing hydrogenase chain vhcG [similarity] - Methanococcus voltae

C/Species: Methanococcus voltae

C/Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004

C/Accession: S32834; S16726

R/Klein, A.

submitted to the EMBL Data Library, August 1991

A/Reference number: S32833

A/Accession: S32834

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-306 <LFE>

A/Cross-references: UNIPROT:Q00406; EMBL:X61203; NID:9296614; PIDN:CAA43505.1; PID:929661

R/Halboth, S.; Klein, A.

submitted to the EMBL Data Library, August 1991

A/Description: Methanococcus voltae harbors two gene groups each of homologous (Nife) - ar

A/Reference number: S16721

A/Accession: S16726

A/Molecule type: DNA

A/Residues: 1-99, 'TA', 102-107, 'P', 126, 'LH', 129-306 <HAL>

A/Cross-references: EMBL:X61203

A/Note: the sequence is revised in Genbank entry X61203, release 117, (PIDN:CAA43505.1)

R/Halboth, S.; Klein, A.

Mol. Gen. Genet. 233, 217-224, 1992

A/Title: Methanococcus voltae harbors four gene clusters potentially encoding two (Nife)

A/Reference number: A59304; MUID:92293118; PMID:1603063

A/Contents: annotation

C/Genetics:

A/Gene: vhcG

C/Superfamily: methyl viologen-reducing hydrogenase gamma chain

Query Match 44.3%; Score 51; DB 2; Length 306;  
Best Local Similarity 46.7%; Pred. No. 21;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 ICRCICTRGFCRCIC 16  
DB 214 VCMGVATRASCRFC 228

## RESULT 7

S58870

reelin precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Dec-1996 #sequence\_revision 06-Dec-1996 #text\_change 21-Jul-2003

C:Accession: S58870; S71844; I49297  
R:ID: Arcangelo, G.; Miao, G.G.; Chen, S.C.; Soares, H.D.; Morgan, J.I.; Curran, T.  
Mature 374, 719-723, 1995  
A:Title: A protein related to extracellular matrix proteins deleted in the mouse mutant  
A:Reference number: I49297; MUID:95231649; PMID:7715726  
A:Accession: S58870  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-3461 <DAR>  
A:Cross-references: EMBL:U24703, NID:9902486, PID:9902487  
R:ID: Arcangelo, G.  
submitted to the EMBL Data Library, April 1995  
A:Reference number: S71844  
A:Accession: S71844  
A:Molecule type: mRNA  
A:Residues: 1-215, 'T', 217-1905, 'S', 1907-3355, 'V', 3357-3391, 'N', 3393-3461 <DA2>  
A:Cross-references: EMBL:U24703, NID:9902486, PID:9902487  
F:1-77/Domain: signal sequence #status predicted <Sig>  
F:28-3461/Product: reelin #status predicted <Mat>  
F:1769-1795/Domain: EGF homology <EGF>

Query Match 43.9%; Score 50.5; DB 2; Length 3461;  
Best Local Similarity 52.6%; Pred. No. 1.3e+02;  
Matches 10; Conservative 1; Mismatches 5; Indels 3; Gaps 1;

OY 1 GIC--RCICTRGFCRCIC 16  
DB 1777 GICDSGRVCYFNDHRCFCGR 1795

RESULT 8

JCS677  
RNA4 protein - Beet necrotic yellow vein mosaic virus  
C:Species: Beet necrotic yellow vein mosaic virus  
C:Date: 11-Nov-1997 #sequence\_revision 11-Nov-1997 #text\_change 09-Jul-2004  
A:Accession: JCS677  
R:Yu, J.L.; Han, C.G.; Yan, L.L.; Li, D.W.; Liu, Y.  
Acta Microbiol. Sin. 37, 7-14, 1997  
A:Title: cDNA cloning, sequence analysis and expression of RNA4 from beet necrotic yellow vein  
A:Reference number: JCS677  
A:Accession: JCS677  
A:Molecule type: mRNA  
A:Residues: 1-282 <YU4>  
A:Cross-references: UNIPROT:O65670

Query Match 43.0%; Score 49.5; DB 2; Length 282;  
Best Local Similarity 42.1%; Pred. No. 30;  
Matches 8; Conservative 1; Mismatches 5; Indels 5; Gaps 1;

OY 5 CICTRGFC----RCICGR 18  
DB 183 CVCSCGVCYFNDHRCFCGR 201

RESULT 9

TIMB  
trypsin inhibitor (Bowman-Birk) - mung bean  
C:Species: Vigna radiata (mung bean)  
C:Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #text\_change 09-Jul-2004  
A:Accession: A01301  
R:Zhang, Y.; Luo, S.; Tan, F.; Qi, Z.; Xu, L.; Zhang, A.  
Sci. Sin. 25, 268-277, 1982  
A:Title: Complete amino acid sequence of mung bean trypsin inhibitor.  
A:Reference number: A01301  
A:Accession: A01301  
A:Molecule type: protein  
A:Residues: 1-72 <ZHA>  
A:Cross-references: UNIPROT:P01062  
A:Note: three isoforms are also found whose amino ends differ slightly from that of  
d Iva-1, respectively  
C:Comment: This inhibitor stoichiometrically inhibits trypsin in a molar ratio of 1:2.  
C:Subfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology  
C:Keywords: duplication; serine proteinase inhibitor

```

F.11-39/Domain Bowman-Birk inhibitor repeat homology <BB1>
F.40-65/Domain Bowman-Birk inhibitor repeat homology <BB2>
F.112-66,13-28,16-62,18-26,36-43,40-55,45-53/Distalide bonds: #status predicted
F.120/inhibitory site: Lys (trypsin) #status predicted
F.147/inhibitory site: Arg (trypsin) #status predicted

Query Match          42.6%; Score 49; DB 1; Length 72;
Best Local Similarity 58.8%; Pred. No. 13;
Matches 10; Conservative 2; Mismatches 1; Indels 4; Gaps 2;

QY      3 CR-CICTR---GFCRCI 15
         |||:|||||
DB       40 CKSCICTRSMPGKCRCL 56

RESULT 10
JC1066
trypsin inhibitor - mung bean
C.Species: Vigna radiata (mung bean)
C.Date: 02-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 18-Aug-2000
C.Accession: JCI066
R.Chen, C.Q.; Mao, J.F.; Zhang, M.F.; Dai, J.F.
Chinese J. Biotechnol. 9, 54-60, 1993
A.Title: Synthesis of mung bean trypsin inhibitor by the combination of the single strand
F.41-66/Domain Bowman-Birk inhibitor repeat homology <BB12>
A.Reference number: JCI066
A.Accession: JCI066
A.Molecule type: DNA
A.Residues: 1-73 <CHE>
C.Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
C.Keywords: serine proteinase inhibitor
F.12-73/Product: trypsin inhibitor #status predicted <MAT>
F.14-40/Domain Bowman-Birk inhibitor repeat homology <BB1>
F.41-66/Domain Bowman-Birk inhibitor repeat homology <BB12>

Query Match          42.6%; Score 49; DB 2; Length 73;
Best Local Similarity 58.8%; Pred. No. 14;
Matches 10; Conservative 2; Mismatches 1; Indels 4; Gaps 2;

QY      3 CR-CICTR---GFCRCI 15
         |||:|||||
DB       41 CKSCICTRSMPGKCRCL 57

RESULT 11
S08167
Babblani ring 3 protein - midge (Chironomus tentans)
C.Species: Chironomus tentans
C.Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Aug-2004
C.Accession: S08167
R.Paulsson, G.; Lendahl, U.; Galli, J.; Ericsson, C.; Wieslander, L.
J. Mol. Biol. 211, 331-349, 1990
A>Title: The babblani ring 3 gene in Chironomus tentans has a diverged repetitive structure
A.Reference number: S08167; MUID:90172404; PMID:1689777
A.Accession: S08167
A.Status: not compared with conceptual translation
A.Molecule type: DNA
A.Residues: 1-1700 <PAU>
A.Cross-references: UNIPROT:Q03376; GB:X52263; NID:g7057; PIDN:CA36506.1; PID:g7058
C.Genetics:
A.Gene: BR3
A.Map position: 4

Query Match          42.6%; Score 49; DB 2; Length 1700;
Best Local Similarity 23.3%; Pred. No. 1,2e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 16; Gaps 1;

QY      3 CRCICTRG-----FCRCIC 16
         |||:|||
DB       1245 CRCVCPKNMEKPADNCCKTKMNDENMCQCVC 1274

RESULT 12
T22945
```

hypothetical protein T01D3.1 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T22945; T24295

R/Pericy, C.

submitted to the EMBL Data Library, October 1996

A/Reference number: Z19640

A/Accession: T22945

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Residues: 1-3191 <M12>

A/Cross-references: UNIPROT:O01335; EMBL:Z81094; PDB:CA803155.1; GSPDB:GN00023; CESP:T01D3.1

A/Experimental source: clone F58G11

R/Steward, C.

submitted to the EMBL Data Library, October 1996

A/Reference number: Z19870

A/Accession: T24295

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Residues: 1-3191 <M12>

A/Cross-references: EMBL:Z81110; PDB:CA803261.1; GSPDB:GN00023; CESP:T01D3.1

A/Experimental source: clone T01D3

C/Genetics:

A/Gene: CESP:T01D3.1

A/Map position: 5

A/Insertions: 18/1; 73/2; 101/3; 241/2; 251/1; 327/3; 383/3; 455/3; 494/1; 793/1; 905/3; 10

Query Match 42.6%; Score 49; DB 2; Length 3191;

Best Local Similarity 30.6%; Pred. No. 1.8e+02;

Matches 11; Conservative 2; Mismatches 1; Indels 22; Gaps 2;

1 GICRC-----ICTR-GFCRC 14

1182 GLCKCEDEMGSRQRCPLCNSCLNGICTRPFSC 1217

Db

RESULT 13

S07405

protease inhibitor (Bowman-Birk) C-II - soybean

C/Species: Glycine max (soybean)

C/Date: 02-Dec-1993 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004

C/Accession: S07405; S29608; S40113

R/Joudrier, P.E.; Foard, D.B.; Floener, L.A.; Larkins, B.A.

Plant Mol. Biol. 10, 35-42, 1987

A/Title: Isolation and sequence of cDNA encoding the soybean protease inhibitors PI IV

A/Reference number: S07405

A/Accession: S07405

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-83 <JOU>

A/Cross-references: UNIPROT:P01063; EMBL:M20732; NID:G169944; PDB:AAA33953.1; PID:G1699

A/Note: the sequences of codons 8-13 and 14-27 are interchanged in the authors' translat

R/Bek, J.M.; Kim, S.I.

submitted to the EMBL Data Library, October 1992

A/Description: Nucleotide sequence of a cDNA encoding the soybean Bowman-Birk proteinase

A/Reference number: S29559

A/Accession: S29559

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-83 <BAE>

A/Cross-references: EMBL:X68705; NID:G18567; PDB:CAA48656.1; PID:G18568

R/Giordano, A.; Delladonne, M.; Fogher, C.; Marchetti, S.

submitted to the EMBL Data Library, December 1993

A/Description: Nucleotide sequence encoding a soybean C-II proteinase inhibitor.

A/Reference number: S40113

A/Accession: S40113

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-83 <GIO>

A/Cross-references: EMBL:X76727; NID:G436413; PDB:CAA54144.1; PID:G436414

C/Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology

C/Keywords: serine proteinase inhibitor

F/22-48/Domain: Bowman-Birk inhibitor repeat homology <BB1>

F/49-74/Domain: Bowman-Birk inhibitor repeat homology <BB12>

Query Match 42.2%; Score 48.5; DB 2; Length 83;

Best Local Similarity 60.0%; Pred. No. 17;

Matches 9; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

4 RCICTR--GFCRCI 15

51 RCACTRSMFGQCRCL 65

Db

RESULT 14

JC2225

Bowman-Birk proteinase isoinhibitor C-II precursor (clone PB24) - soybean

C/Species: Glycine max (soybean)

C/Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 18-Aug-2000

C/Accession: JC2225

R/Bek, J.M.; Song, J.C.; Choi, Y.D.; Kim, S.I.

Biochem. Biotechnol. Biochem. 58, 843-846, 1994

A/Title: Nucleotide sequence homology of cDNAs encoding soybean Bowman-Birk type proteinase

A/Reference number: JC2224; MUID:94289861; PMID:7764974

A/Accession: JC2225

A/Molecule type: mRNA

A/Residues: 1-94 <BAE>

A/Comment: This protein regulates endogenous proteinase during germination, stores sulfa

C/Genetics:

A/Start codon: GTT

C/Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology

C/Keywords: duplication; seed; serine proteinase inhibitor

F/1-18/Domain: signal sequence #status predicted <SIG>

F/19-94/Product: Bowman-Birk proteinase isoinhibitor C-II #status predicted <MAT>

F/33-59/Domain: Bowman-Birk inhibitor repeat homology <BB1>

F/60-85/Domain: Bowman-Birk inhibitor repeat homology <BB12>

Query Match 42.2%; Score 48.5; DB 2; Length 94;

Best Local Similarity 60.0%; Pred. No. 18;

Matches 9; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

4 RCICTR--GFCRCI 15

62 RCACTRSMFGQCRCL 76

Db

RESULT 15

TISYC2

protease inhibitor (Bowman-Birk) C-II precursor - soybean

C/Species: Glycine max (soybean)

C/Date: 24-Apr-1984 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C/Accession: A22636; A01302

R/Hammond, R.W.; Foard, D.B.; Larkins, B.A.

J. Biol. Chem. 259, 9883-9890, 1984

A/Title: Molecular cloning and analysis of a gene coding for the Bowman-Birk proteinase int

A/Reference number: A92489; MUID:84264652; PMID:6086657

A/Contents: annotation

A/Note: the sequence has been revised in reference A92540

R/Hammond, R.W.; Foard, D.B.; Larkins, B.A.

J. Biol. Chem. 260, 7806, 1985

A/Reference number: A92540

A/Contents: erratum

A/Accession: A22636

A/Molecule type: DNA

A/Residues: 1-103 <HAM>

A/Cross-references: UNIPROT:P01063; GB:X01967; NID:G169942; PDB:AAA33952.1; PID:G169943

R/Ogami, S.; Ikenaka, T.

J. Biochem. 82, 1523-1531, 1977

A/Title: Studies on soybean trypsin inhibitors. XI. Complete amino acid sequence of a soy

A/Reference number: A01302; MUID:78087480; PMID:599141

A/Accession: A01302

A/Molecule type: protein

A/Residues: 28-103 <ODA>

A/Comment: This protein inhibits trypsin, elastase, and chymotrypsin. The site of interac

C/Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology

C/Keywords: duplication; seed; serine proteinase inhibitor



F;1-27/Domain: signal sequence #status predicted <SIG>  
F;28-103/Product: proteinase inhibitor (Bowman-Birk) C-II #status experimental <MAT>  
F;42-68/Domain: Bowman-Birk inhibitor repeat homology <BB1>  
F;59-94/Domain: Bowman-Birk inhibitor repeat homology <BB2>  
F;41-95,42-57,45-91,47-55,65-72,69-84,74-82/Disulfide bonds: #status predicted  
F;49/Inhibitory site: Ala (elastase) #status predicted  
F;76/Inhibitory site: Arg (trypsin) #status experimental

Query Match 42.2% Score 48.5; DB 1; Length 103;  
Best Local Similarity 60.0%; Pred. No. 20;  
Matches 9; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy 4 RCICTR---GFCRCI 15  
Db 71 RCACTRSMPGQCRL 85

Search completed: March 22, 2005, 20:50:38  
Job time : 48 secs

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1	64	55.7	76	1	TDLA_MACHU
2	61.5	53.5	168	2	O87BL8
3	58.5	50.9	83	2	Q7PGC24
4	58	50.4	168	2	O6P8T4
5	58	50.4	168	2	O8CHN20
6	58	50.4	168	2	O9DP912
7	58	50.4	168	2	O9D4K2
8	57.5	50.0	377	2	O9G282
9	56.5	49.1	163	2	O8VJZ20
10	55	47.8	166	2	Q7OBV4
11	55	47.8	1823	3	Q7RPS5
12	54.5	47.4	190	2	O9IU123
13	54.5	47.4	307	2	O8H9U3
14	54	47.0	193	2	O8S6V3
15	54	47.0	201	2	O6ZDS2
16	54	47.0	609	2	Q7GXN8
17	53.5	46.5	379	2	O7SXOV
18	53	46.1	336	2	Q7PVN9
19	53	46.1	657	2	Q7OYH8
20	53	46.1	1365	2	Q7SNR8
21	53	46.1	2871	2	Q7SN87
22	52.5	45.7	129	2	Q7F070
23	52.5	45.7	512	2	O6R9J9
24	52.5	45.7	289	2	BFN3_HUMAN
25	52.5	45.7	3008	2	O6QLI44
26	52	45.2	112	2	O9UT45
27	52	45.2	274	2	O949G1
28	52	45.2	848	2	O93U55
29	51.5	44.8	101	2	Q7YUJ2
30	51.5	44.8	118	2	O8CGN2
31	51.5	44.8	131	2	O9D261
P22270	maccia mula				
O87B18	xylella fas				
Q7PGC24	anopheles g				
O6P8T4	mus musculus				
O8CHN20	mus musculus				
O9DP912	mus musculus				
O9D4K2	mus musculus				
O9G282	mus musculus				
O8VJZ20	mycobacteri				
Q7OBV4	anopheles g				
Q7RPS5	anopheles g				
O9IU123	hom sapien				
O8H9U3	hom sapien				
O8S6V3	coryza sativ				
O6ZDS2	hom sapien				
Q7GXN8	glardia lam				
O7SXOV	brachydanio				
Q7PVN9	anopheles g				
Q7OYH8	glardia lam				
Q7SNR8	hom sapien				
Q7SN87	hom sapien				
Q7F070	anopheles g				
O6R9J9	rattus norv				
BFN3_HUMAN	hom sapien				
O6QLI44	bos taurus				
O9UT45	tendbrio mo				
O949G1	coryza sativ				
O93U55	carsonella				
Q7YUJ2	trypanosoma				
O8CGN2	mus musculu				
O9D261	mus musculu				

32	51.5	44.8	160	2	Q6H654	Q6H654	homo sapien
33	51.5	44.8	243	2	Q6ZMP3	Q6ZMP3	homo sapien
34	51.5	44.8	462	2	Q6GQP2	Q6GQP2	brachydanio
35	51	44.3	82	2	Q7PKA1	Q7PKA1	anopheles g
36	51	44.3	142	2	Q8NAA0	Q8NAA0	homo sapien
37	51	44.3	164	2	Q22048	Q22048	caenorhabdi
38	51	44.3	166	2	Q95QY1	Q95QY1	caenorhabdi
39	51	44.3	188	2	Q18238	Q18238	caenorhabdi
40	51	44.3	197	2	Q17641	Q17641	caenorhabdi
41	51	44.3	306	1	VHGC_METWO	Q00406	methanococc
42	51	44.3	602	2	Q7SNZ5	Q7SNZ5	chlamydomon
43	51	44.3	937	1	Q9BLJ1	Q9BLJ1	ciona intest
44	51	44.3	4599	1	LR1B_MOUSE	Q9J118	mus musculi
45	50.5	43.9	94	2	Q8COH3	Q8COH3	mus musculi

## ALIGNMENTS

ID	TDLA_MACMU	STANDARD;	PRT;	76 AA.
AC	P82270; QSTU01;			
BT	25-OCT-2004 (Rel. 45, Created)			
DT	25-OCT-2004 (Rel. 45, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Theta defensin-1, subunit A precursor (RTD-1a) (Demicdefensin 2).			
GN	Name=RTD1a;			
OS	Macaca mulatta (Rhesus macaque).			
OC	Eukaryota; Metazoa; Chordata; Crinata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecoidea; Macaca.			
OX	NCBI_TaxID=95544;			
RN	[1]			
RP	SEQUENCE FROM N.A., SEQUENCE OF 65-73, TISSUE SPECIFICITY,			
RP	DEVELOPMENTAL STAGE, AND DISULFIDE BONDS.			
RC	TISSUE=Bone marrow, and Leukocyte;			
RX	MEDLINE=99453140; Pubmed=10521339; DOI=10.1126/science.286.5439.498;			
RA	Tang Y.-Q., Yuan J., Oesapay G., Oesapay K., Tran D., Miller C.J.,			
RA	Cyellette A.J., Selsted M.E.;			
RT	"A cyclic antimicrobial peptide produced in primate leukocytes by the			
RL	ligation of two truncated alpha-defensins.";			
RL	Science 286:498-502(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	Zhao C., Nguyen T., Lehrer R.I.;			
RT	"cDNA cloning of three alpha-defensins and three demidefensins from			
RT	rhesus monkey bone marrow.";			
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: Active against the Gram-positive bacteria <i>S.aureus</i> and			
CC	<i>L.monocytogenes</i> , Gram-negative bacteria <i>S.typhimurium</i> and <i>E.coli</i>			
CC	<i>M.35</i> and fungi <i>C.abicans</i> and <i>C.neoformans</i> in vitro.			
CC	-1- SUBUNIT: Forms a cyclic heterodimer composed of subunits A and B;			
CC	disulfide-linked.			
CC	-1- TISSUE SPECIFICITY: Expressed in bone marrow. Detected in			
CC	promyelocytes, myelocytes and mature neutrophils and monocytes.			
CC	-1- DEVELOPMENTAL STAGE: Expression begins early during granulocyte			
CC	myelopoiesis.			
CC	-1- PTM: This is a cyclic peptide.			
CC	-1- SIMILARITY: Belongs to the corticostatin/defensin family.			
CC				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See <a href="http://www.1db-sib.ch/announce/">http://www.1db-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL; AF191100; AAF04389.1; -			
DR	EMBL; AF191102; AAF04391.1; -			
DR	EMBL; AF194157; AAF07924.1; -			

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DR   PIR; A59089; A59089.
DR   InterPro; IPR002366; Defensin_propep.
DR   Pfam; PF00879; Defensin_propep; 1.
DR   PROSITE; PS00269; DEFENSIN; FALSE NEG.
KW   Antibiotic; Defensin; Direct protein sequencing; Fungicide; Signal.
FT   SIGNAL      1 22
FT   PROPEP      23 73
FT   PEPTIDE      65 73      Theta defensin-1, subunit A.
FT   PROPEP      74 76
FT   DISULFID     66 66      Interchain (with C-66 of subunit B).
FT   DISULFID     68 73
FT   CONFLICT     38 38
SQ   SEQUENCE     76 AA; 8282 MW; BE207932A030590 CRC64;

Query Match      55.7%; Score 64; DB 1; Length 76;
Best Local Similarity 83.3%; Pred. No. 0.47;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY   4 RCICITRGFCRCI 15
DB   65 RCICITRGFCRL 76

RESULT 2
Q87BL8 PRELIMINARY; PRT; 168 AA.
AC   Q87BL8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocNames=PD1431;
OS   Xylella fastidiosa (strain Temecula / ATCC 700964).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC   Xanthomonadaceae; Xylella.
OX   NCBI_TaxID=183190;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   DOI=10.1128/JB.185.3.1018-1026.2003;
RA   Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
RA   Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,
RA   Taktla M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
RA   Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorri H., Tsai S.M.,
RA   Carier H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
RA   Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,
RA   Marino C.L., Gaglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
RA   Baia G.S., Bianco S.R., Brito M.S., Camayan F.S., Celestino A.V.,
RA   da Cunha A.F., Penille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
RA   Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sasaki F.T., Sena J.A.D.,
RA   de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zartos L.G.,
RA   Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
RA   Kitajima J.P.;
RT   "Comparative analyses of the complete genome sequences of Pierce's
RT   disease and citrus variegated chlorosis strains of Xylella
RT   fastidiosa."
RL   J. Bacteriol. 185:1018-1026(2003).
DR   EMBL; AE012558; AA029277.1; -.
KW   Complete proteome.
SQ   SEQUENCE 168 AA; 17967 MW; 87A25F3C5E818C8 CRC64;

Query Match      53.5%; Score 61.5; DB 2; Length 160;
Best Local Similarity 50.0%; Pred. No. 1.8;
Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY   1 GICRCITRGFCRCIGR 18
DB   144 GVCCTCCVCG---CVCQG 158

RESULT 3
Q7PG24 PRELIMINARY; PRT; 83 AA.

```

```

AC   Q7PG24;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ENSANGP00000023115.
GN   Name=ENSANG00000021478;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PEST;
RA   Anopheles Genome Sequencing Consortium;
RL   Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC   -1 CAUTION: The sequence shown here is derived from an
CC   EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC   preliminary data.
DR   EMBL; AAB01008846; EAA45095.1; -.
SQ   SEQUENCE 83 AA; 9462 MW; 7F4B67437A0B5EB4 CRC64;

Query Match      50.9%; Score 58.5; DB 2; Length 83;
Best Local Similarity 47.1%; Pred. No. 2.5;
Matches 8; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY   2 ICRCITRGFCRCIGR 18
DB   69 VCVVCV---CMVCVGR 82

RESULT 4
Q6P8T4 PRELIMINARY; PRT; 168 AA.
AC   Q6P8T4;
ID   Q6P8T4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   4931420D14R1k protein.
GN   Name=4931420D14R1k protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Scheef C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein W.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallory S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
RA   Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smallos D.E., Scherck A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences."
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
DR   EMBL; BC061079; AAH61079.1; -.

```

QY	SEQUENCE	168 AA;	18947 MW;	B00FD3D27B9BF768 CRC64;
QY	Query Match	50.4%;	Score 58;	DB 2;
QY	Best Local Similarity	56.2%;	Pred. No. 5.1;	Length 168;
QY	Matches	9;	Conservative 0;	Mismatches 7; Indels 0; Gaps 0;
DB	66	CRCCCYCRCCCRCCSR	81	
RESULT 5				
Q8CH20	PRELIMINARY;	PRT;	168 AA.	
AC	Q8CH20;			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE	Basic protein CK1R3.			
CN	Name=4931420D14R1k; Synonyms=Ckt1r3;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Testis;			
RC	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;			
RA	Carninci P., Hayashizaki Y.;			
RT	"High-efficiency full-length cDNA cloning.";			
RT	Mech. Enzymol. 303:19-44(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Testis;			
RC	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;			
RA	Carninci P., Hayashizaki Y.;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			
RT	Nature 409:685-690(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
Q9D912	PRELIMINARY;	PRT;	168 AA.	
AC	Q9D912;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700065105 product:hypothetical Cyteline-rich region			
DE	containing protein, full insert sequence.			
CN	Name=4931420D14R1k;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Testis;			
RC	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;			
RA	Carninci P., Hayashizaki Y.;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			
RT	Nature 409:685-690(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
Q9D912	PRELIMINARY;	PRT;	168 AA.	
AC	Q9D912;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700065105 product:hypothetical Cyteline-rich region			
DE	containing protein, full insert sequence.			
CN	Name=4931420D14R1k;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Testis;			
RC	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;			
RA	Carninci P., Hayashizaki Y.;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			
RT	Nature 409:685-690(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
Q9D912	PRELIMINARY;	PRT;	168 AA.	
AC	Q9D912;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700065105 product:hypothetical Cyteline-rich region			
DE	containing protein, full insert sequence.			
CN	Name=4931420D14R1k;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Testis;			
RC	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S			

RC	STRAIN=C57BL/6J; TISSUE=Testis;
RA	The PANTOM Consortium,
RB	the RIKEN Genome Exploration Research Group Phase I & II Team;
RC	"Analysis of the mouse transcriptome based on functional annotation of
RD	60,770 full-length cDNAs.";
RE	Nature 420:563-573(2002)."
RF	
RG	
RH	
RI	
RJ	
RK	
RL	
RM	
RN	
RO	
RP	SEQUENCE FROM N.A.
RQ	STRAIN=C57BL/6J; TISSUE=Testis;
RS	MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RT	Shibata K., Itoh M., Atzawa K., Nagaoaka S., Sasaki N., Carninci P.,
RU	Kono H., Akiyama J., Nishi K., Kitenuma T., Tashiro H., Itoh M.,
RV	Sunni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RW	Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kasaiwagi K.,
RX	Fujiwara S., Inoue K., Togawa K., Izawa M., Ohara E., Matshiki M.,
RY	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RZ	Okazaki Y., Muramatsu M., Inoue Y., Kir A., Hayashiaki Y.;
SA	"RIKEN integrated sequence analysis (RISA) system-384-format
SB	sequencing pipeline with 384 multicapillary sequencer.";
SC	Genome Res. 10:1757-1771(2000).
SD	[6]
SE	SEQUENCE FROM N.A.
SF	STRAIN=C57BL/6J; TISSUE=Testis;
SG	Adachi J., Atzawa K., Akahira S., Akimura T., Arai A., Aono H.,
SH	Arikawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
SI	Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirakawa T., Horii F.,
SJ	Inomati K., Ishii Y., Itoh M., Izawa M., Kasutawa T., Kato H.,
SK	Kawai J., Koizumi Y., Kono H., Kouda M., Koya S., Kurihara C.,
SL	Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numasaki R., Ono M.,
SM	Okazaki Y., Okido T., Owa C., Salto R., Salto R., Sakai K., Sakai K.,
SN	Sano H., Saeki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
SO	Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
SP	Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
SQ	Muramatsu M., Hayashizaki Y.;
SR	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
SS	EMBL; AK006892; BAB24782.1;"
ST	GMD; MG1:1913992; 4931420D1ARLK.
SV	Hypothetical protein..
SW	SEQUENCE 168 AA; 18931 MW; 7A2BD279612A5B94 CRC64;
SX	
SY	
SY	Query Match 3 CRCTCTRGFCRCITCGR 18
SY	Best Local Similarity 50.4%; Score 58; DB 2; Length 168;
SY	Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
DB	66 CRCCCHCRCCRCCCSR 81
RESULT 7	
Q9DAK2	PRELIMINARY; PRT; 173 AA.
AC Q9DAK2;	
DT 01-JUN-2001 (TREMBLrel. 17, Created)	
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)	
DE 01-OCT-2002 (TREMBLrel. 22, last annotation update)	
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched	
DE library, clone:931420D14 product:hypothetical cysteine-rich region	
DE containing protein, full insert sequence.	
GN Name=4931420D14R1k;	
OS Mus musculus (Mouse);	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
NCBI TaxID=10090;	

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RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA "RIKEN FANTOM Consortium";
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN (4)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subcloning of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN (5)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Iehi Y., Nakamura S., Hazama M., Nishire T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujitake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Oneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN (6)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imocani K., Iehi Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numata K., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai T.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toyota T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK016467; BAB30253.1;
DR MGD; MGI:1913992; 4931420D14Rik.
KW Hypothetical protein.
SO SEQUENCE 173 AA; 19581 MW; 147BEF155AC29PDF CRC64;

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Query Match 50.4%; Score 58; DB 2; Length 173;
Best Local Similarity 56.2%; Pred. No. 5.2;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3 CRCTCTRGFCRCICGR 18
DB 66 CRCCCTCCRCRCRCSR 81

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RESULT 8
O96282 PRELIMINARY; PRT; 307 AA.
AC O96282;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein PFB0950W.
GN Name=PFB0950W;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=99021743; PubMed=9804551; DOI=10.1126/science.282.5391.1126;
RA Gardner M.J., Tettein H., Carucci D.J., Cummings L.M., Aravind L.,
RA Koonin E.V., Shallow S., Mason T., Yu K., Fujii C., Peterson J.,
RA Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Perera M.,
RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Science 282:1126-1132(1998).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Bain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyte S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Perera M., Allen J., Selengut J., Haft D., Mather M.W., Valdivia A.B.,
RA Martin D.M.A., Fairhead A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrett I.B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE001428; AAC71979.2;
DR PIR; E71602; E71602.
DR HSSP; P01056; I134.
DR INTERPRO; IPR001368; TNFR_C6.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
KW Hypothetical protein.
SO SEQUENCE 307 AA; 35537 MW; B95A3DB354D4BE71 CRC64;

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Query Match 50.0%; Score 57.5; DB 2; Length 307;
Best Local Similarity 66.7%; Pred. No. 9.6;
Matches 10; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
QY 2 ICRCCTRGFCRCIC 16
DB 221 ICSCICT--CTCIC 232

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RESULT 9
O8VJ20 PRELIMINARY; PRT; 163 AA.
AC O8VJ20;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=MT13454;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;

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RX DOI=10.1128/JB.184.19.5479-5490.2002;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.D., Deboy R.T., Dodson J.J., Gwin M.L., Haft D.H.,
RA Hickey E.K., Kolony J.F., Nelson W.C., Umayam L.A., Ermakova M.D.,
RA Salzberg S.L., Delcher A., Ueberck T.R., Weidman J.F., Kouri H.M.,
RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).
DR EMBL: AE000516; AAK4795.1; -.
DR TIGR: MT3454; -.
KM Hypochemical protein.
SQ SEQUENCE 163 AA; 18621 MW; B5E62AB951B2AC3C CRC64;

Query Match 49.1%; Score 56.5; DB 2; Length 163;
Best Local Similarity 60.0%; Pred. No. 7.6;
Matches 9; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

OY 3 CRCICTR-GFRCIC 16
DB 137 CRHVCTRSYCRVLC 151

RESULT 10
ID Q7QBVA PRELIMINARY; PRT; 146 AA.
AC Q7QBVA;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AGCP1494 (Fragment).
GN Name=agcC47401; ORFNames=ENSANG000000012913;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RL Anopheles Genome Sequencing Consortium;
CC Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAB01008859; EAA07639.1; -.
DR NON_TER 1
FT SEQUENCE 146 AA; 16746 MW; 7D32B8AABE776F98 CRC64;

Query Match 47.8%; Score 55; DB 2; Length 146;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 5 CICTRGFCRCIC 17
DB 44 CVCVLGWCRCVCG 56

RESULT 11
ID Q7PRPS PRELIMINARY; PRT; 1823 AA.
AC Q7PRPS;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP00000019046 (Fragment).
GN Name=ENSANGG00000016557;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAB01008847; EAA06854.2; -.
DR HSSP: P00740; 1EDM.
DR InterPro: IPR00152; Asx_hydroxyl_5.
DR InterPro: IPR008985; Con_1like_1ec_1.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR009030; Grow_fac_recept.
DR InterPro: IPR003410; Hyalinin_G.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR001759; Pentaxin.
DR InterPro: IPR001211; PhospholipaseA2.
DR InterPro: IPR000436; Sushi_SCR_CCP.
DR InterPro: IPR002035; VWF_A.
DR Pfam: PF00008; EGF_5.
DR Pfam: PF02494; HVR_2.
DR Pfam: PF00354; Pentaxin; 1.
DR Pfam: PF00084; Sushi; 5.
DR Pfam: PF00092; VMA; 1.
DR PRINTS: PR00895; PENTAXIN.
DR PRINTS: PR00453; VWFADOMAIN.
DR ProDom: PD002153; Pentaxin; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_5.
DR PROSITE: PS01186; EGF_2; 4.
DR PROSITE: PS50026; EGF_3; 5.
DR PROSITE: PS50825; HVR_2.
DR PROSITE: PS50025; LAM_G_DOMAIN; 1.
DR PROSITE: PS00118; PA2_HIS; UNKNOWN_1.
DR PROSITE: PS50923; SUSHI; 8.
DR PROSITE: PS50234; VWF_A; 1.
FT NON_TER 1
FT NON_TER 1823
FT SEQUENCE 1823 AA; 200582 MW; 5740C4C700804379 CRC64;

Query Match 47.8%; Score 55; DB 2; Length 1823;
Best Local Similarity 53.3%; Pred. No. 85;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 ICRCICRGFCRCIC 16
DB 262 VCSCLTSGHYRCIC 276

RESULT 12
ID Q9UI23 PRELIMINARY; PRT; 190 AA.
AC Q9UI23;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE PRO0529.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Zhang C., Yu Y., Zhang S., Ouyang S., Luo L., Wei H., Zhou G.,
RA Zhang Y., Liu M., He F.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF11848; ARI1687.1; -.
DR SEQUENCE 190 AA; 21480 MW; 4B8104A29AA33844 CRC64;

Query Match 47.4%; Score 54.5; DB 2; Length 190;
Best Local Similarity 44.4%; Pred. No. 15;
Matches 8; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

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QY 2 ICRCTCTRG---FCRCIC 16  
 Db 47 VCLCMCTGCGVSVCCVC 64

RESULT 13  
 Q9H9U3 PRELIMINARY; PRT; 307 AA.

AC Q9H9U3;  
 DT 01-MAR-2001 (TEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)  
 DE Hypochemical protein FLJ12547.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxId=9606;  
 RX PubMed=14702039; DOI=10.1038/ng1285;  
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
 RA Sekine M., Ohyashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,  
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,  
 RA Sudo H., Hosioki T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Takahashi N., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,  
 RA Abe K., Kamihara K., Katsuma N., Sato K., Tanikawa M., Yamazaki M.,  
 RA Ninomiya K., Ihibashi T., Yamashita H., Murakawa K., Fujimori K.,  
 RA Tanai H., Kimura M., Watanabe M., Hirooka S., Chiba Y., Ishida S.,  
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,  
 RA Togiyasu S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,  
 RA Musashino K., Yuki H., Oshima A., Sasaki N., Aocuka S.,  
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,  
 RA Moriya S., Komiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
 RA Hishigaki H., Watanabe T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiro M., Ohnori Y.,  
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
 RA Matsunawa K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Maehuo Y., Yamashita R.,  
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,  
 RT "Complete sequencing and characterization of 21,243 full-length human  
 RT cDNAs".  
 RL Nat. Genet. 36:40-45(2004).  
 DR EMBL: AK022609; BAB14128.1; -  
 SQ SEQUENCE 307 AA; 32780 MW; 4CC18ACD39BD3AC3 CRC64;

Query Match 47.4%; Score 54.5; DB 2; Length 307;  
 Best Local Similarity 42.1%; Pred. No. 23;  
 Matches 8; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

QY 2 ICRCTCTRG---FCRCIC 17  
 Db 100 VCACVCGCTFVCACVCG 118

RESULT 14  
 Q8S6V3 PRELIMINARY; PRT; 193 AA.

AC Q8S6V3;  
 DT 01-JUN-2002 (TEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)  
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)  
 DE Hypochemical protein OSJNB0014J14.16.  
 GN ORFNames=OSJNB0014J14.16;

OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 NCBI\_TaxId=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wang R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,  
 RA Sasaki C., Henry D., Oates R., Simmons J.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA The Rice Chromosome 10 Sequencing Consortium;  
 RT "in-depth view of structure, activity, and evolution of rice  
 RT chromosome 10".  
 RL Science 300:1566-1569(2003).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Buell C.R., Wang R.A., McCombie W.R., Messing J., Yuan Q.,  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC092172; AAM18156.1; -  
 DR EMBL: AB017071; AAP2751.1; -  
 DR Gramene: Q8S6V3; -  
 DR InterPro: IPR006209; EGF like.  
 DR PROSITE: PS01186; EGF\_2; UNKNOWN\_1.  
 KW Hypochemical protein.  
 SQ SEQUENCE 193 AA; 20366 MW; B5204B4526E5A769 CRC64;

Query Match 47.0%; Score 54; DB 2; Length 193;  
 Best Local Similarity 61.1%; Pred. No. 18;  
 Matches 11; Conservative 1; Mismatches 4; Indels 2; Gaps 2;

QY 1 GICRCICTRG-FCRCIC 17  
 Db 145 GGCRCGCGGCGC-CG 161

RESULT 15  
 Q6Z0S2 PRELIMINARY; PRT; 201 AA.

AC Q6Z0S2;  
 DT 05-JUL-2004 (TEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)  
 DE Hypochemical protein FLJ45585.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TRISUB=Thalamus;  
 RA Kanehori K., Ishihashi T., Chiba Y., Fujimori K., Hirooka S.,  
 RA Tanai H., Watanabe S., Ishida S., Ono Y., Houta T., Watanabe M.,  
 RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,  
 RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,  
 RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,  
 RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,  
 RA Suzuki Y., Sugano S., Nagahari K., Maehuo Y., Nagai K., Isogai T.,  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK128797; BAC87611.1; -  
 DR InterPro: IPR006209; EGF like.  
 DR PROSITE: PS01186; EGF\_2; UNKNOWN\_1.  
 SQ SEQUENCE 201 AA; 20938 MW; 3408F8E817AA0500 CRC64;

Query Match 47.0%; Score 54; DB 2; Length 201;  
 Best Local Similarity 40.0%; Pred. No. 19;  
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 ICRCTCTRGFCRCIC 16  
 Db 58 VCLCVLVSVCCVC 72



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Search completed: March 22, 2005, 20:49:45  
Job time : 175 secs

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